



PATENT  
Attorney Docket No. NREL 01-35:  
Express Mail Label No. *712*

THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Ding et al.

Examiner: Manjunath Rao

Serial No. 09/917,378

Group Art Unit: 1652

Filed: July 28, 2001

Confirmation No. 9985

For: THERMAL TOLERANT  
MANNANASE FROM  
ACIDOTHERMUS  
CELLULOLYTICUS

RECEIVED

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Box: FEE AMENDMENT  
Commissioner for Patents  
Washington, DC 20231

Sir:

**DECLARATION OF SHI-YOU DING, Ph.D**

**37 C.F.R. §1.132**

1. I am the Shi-You Ding who is named as an inventor in the above-identified application.
2. Exhibit A to this Declaration is my curriculum vitae. I am currently employed at the National Renewable Energy Laboratory in Golden, Colorado where I work as a Senior Research Scientist. I have many years of bench research experience in the field of microbiology with focus in hydrolyzing enzymes.
3. This declaration is provided with evidence that refutes certain of the Examiner's arguments in the Office Action dated January 10, 2003.
4. The first issue is to address the arguments beginning on page 7 and which concern the rejection of claims 1-5 and 12-13 because the specification allegedly does not enable claims this broad. For the reasons explained below, this cannot be the case where the claims identify well known families of domains.
5. Exhibit B to this Declaration contains an excerpt of information that is published in the CAZy database (cited as Coutinho, P.M. & Henrissat, B. (1999)

Carbohydrate-Active Enzymes server at URL: <http://afmb.cnrs-mrs.fr/~cazy/CAZY/index.html>). CAZy was produced over a ten year period and contains cross-linkages to a variety of international sequence databases. The "Family GH5" domains extend from pages 1 to 13 of Exhibit B. The Family CBDIII domains extend from pages 16 to 18. The "Family CBDII domains extend from pages 19-22.

6. Scientists who practice in my field are routinely trained in the use of computer databases, such as the CAZy, GenBank, and SwissProt databases identified in Exhibit B. The mere mention that a particular poly[peptide domain is classified in of one of these families causes an instant recognition that the domain is in a similar classification with respect to other domains in that family. The ability to access domains by this classification system is a fundamental and basic part of our working knowledge.

7. Therefore, it is simply not correct for the Examiner to say that the specification fails to disclose the multiple modifications encompassed by the instant claims. Multiple modifications are, in fact, disclosed by the domain family names. Those skilled in the art appreciate from the disclosure in the specification that these well known family domains may be linked together in perhaps thousands of permutations of GH5-CBDIII-CBDII domains. Furthermore, molecular genetics are sufficiently advanced that those following the disclosure of the present specification would routinely be able to make such linkages.

8. It follows that the allegations raised as points A through E in the passage bridging pages 8-9 are false. The specification does disclose a specific guidance and rationale for practicing the claimed invention when it refers to the domain family names.

9. Another issue is that on page 15 of the Office Action the Examiner has shifted the burden to Applicants to prove that Gibbs et al., Appl. Environ. Microbiol. 58(12) 3864-3867 (1992) does not contain linked GH5-CBHIII-CBHII domains.

10. Exhibit C to this Declaration is an excerpt from the Swiss Prot database, and it contains a summary of the sequence reported by Gibbs. The middle portion of page 2 thereof contains a summary of the domains.

11. I have studied Exhibit C to classify the domains identified on page 2 thereof. Handwritten comments of "GH5," "CBDII," and "CBDII" indicate my conclusion that Gibbs teaches a sequence of GH5-CBDII-CBDII family domains. This is not the sequence of GH5-CBDIII-CBDII that is presently recited in claim 1.

12. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under 18 U.S.C. § 1001, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 4-22-03

By: Shi-You Ding

Shi-You Ding, Ph.D

# SHI-YOU DING *Ph.D*

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## EDUCATION

<b>Postdoctoral fellow</b> , The Weizmann Institute of Science & Tel Aviv University, Israel	1997-2000
<b>Ph.D</b> , Peking University & The Chinese Academy of Sciences, China	1994
<b>M.S.</b> The Chinese Academy of Sciences, China	1989
<b>B.Sc.</b> Anhui Normal University, China	1986

## MEMBERSHIPS

American Society of Microbiology, American Chemical Society

## PROFESSIONAL EXPERIENCE

<b>Scientist II</b> , National Renewable Energy Laboratory	2002-present
<b>Research associate</b> , National Renewable Energy Laboratory	2000-2001

**Nanotechnology.** Understanding Nanoscale Chemistry: Quantum Dot Interactions with Proteins and Carbon Nanotubes and the Mediation of Inter-Quantum Dot Communication.

- ❖ Cloned and expressed clostridia cellulosomal scaffoldin proteins
- ❖ Making protein/quantum dot conjugates
- ❖ Making quantum dots arrays by scaffoldin protein templates.

**Cellulase Fundamentals.** Biochemistry and molecular biology of enzyme system of cellulytic organism

- ❖ Cloned, sequenced four Glycoside Hydrolase genes from *Acidothermus cellulolyticus*. Four ROIs have been filed.
- ❖ Developed *E. coli* system for *Acidothermus* enzyme expression. Six catalytic domain of *Acidothermus* enzymes have been expressed and purified.
- ❖ Set up sequence database of CBHs (Family 7 cellulase), aligned the sequences of all available Family 7 cellulase, designed degenerate PCR primers for screening new CBHs from potential microorganisms.
- ❖ Assisted to identify new CBHs found from *Penicillium sp.* and other cellulose degraders, designed PCR primers for further gene cloning.

**CBHI Expression.** Evaluate the CBHI expression in different system, e.g. *E. coli*, fungi and insect cells.

- ❖ Cloned the catalytic domain of *T. reesei* CBHI into different expression vectors, including pET22b, pET32b, pET40b, pMAL-p2, generated ten CBHI-cd expression constructs, with or without signal sequences, fusion proteins, and tags.
- ❖ Expressed CBHI constructs in *E. coli* strains, including XL-1blue, BL21, BL21(DE3), BL21 *trx* (DE3), BL21(DE3)pLysS, Origami(DE3), Origami(DE3)pLysS, tested the expression level.
- ❖ Cloned CBHI-cd into a *E. coli* -fungi shuttle vector pPFE1 with or without 6xHis tag, prepared the constructs for expression CBHI-cd in fungi.

### Co-PI proposals

- ❖ **DOE Office of Science National Nanotechnology Initiative:** Understanding Nanoscale Chemistry: Quantum Dot Interactions with Proteins and Carbon Nanotubes and the Mediation of Inter-Quantum Dot Communication. PI: Arthur J. Nozik  
\* This proposal has been funded at a level of \$750k/yr.
- ❖ **NASA OLMSA Microgravity Research Division:** Self-assembling Proteins: new Superlattice Structures for Efficient Electro-optic Devices. PI: Mike E. Himmel.
- ❖ **DOE Office of Science Microbial Cell Project:** Toward Understanding the Clostridial Cellulosome: A Bioinformatics Approach. PI: Mike E. Himmel.
- ❖ **DDRD:** Preparation and Characterization of Novel Quantum Dot/Protein Conjugates. PI: Mike E. Himmel & Garry Rumbles.

DOE Microbial Cell Project Review Panel (June 2001).

**Postdoctoral fellow**, The Weizmann Institute of Science & Tel Aviv University, Israel

1997-1999

- ❖ Identified high-molecular-weight (200-400 kDa) cellulosome-related proteins, including scaffolding proteins and cell surface anchoring proteins, from different cellulolytic bacteria.
- ❖ Constructed genomic libraries. Five genes encoding cellulosome-related protein, 6-12kb in size, were cloned from *Acetivibrio celiulolyticus*, *Bacteroides cellulosolvens*, and *Ruminococcus flavefaciens* (collaborated with Dr. Harry J. Flint, Rowett Research Institute, UK), respectively.
- ❖ Expressed and purified three functional domains.
- ❖ Crystallized and determined the crystal structure of CBD from *Clostridium cellulolyticum* scaffolding protein (collaborated with Dr. Linda Shimon et al. at The Weizmann Institute of Science).
- ❖ Crystallization of cohesin domains from *B. cellulosolvens*, *Ruminococcus flavefaciens*, and co-crystal of cohesin domain of scaffoldin and dockerin domain of catalytic subunit from *C. thermocellum* are still under processing.

**Assistant Investigator**, Peking University, China

1995-1996

- ❖ Cloning, and expression of plant resistance genes and molecular biology of Rice Dwarf Virus.
- ❖ DNA fragments isolation from ancient materials.
- ❖ Molecular evolution and systematics of Astragalinae.
- ❖ Constructed the local molecular biological database and the Homepage of the laboratory

**Visiting Research Fellow**, Peking University

1993-1994

- ❖ Molecular phylogenetic study on Astragalinae

**Research Assistant**, The Chinese Academy of Sciences

1989-1994

- ❖ Ecological investigation in wild field, specimen identification in herbarium
- ❖ Cladistic analysis of Astragalinae based on morphological and ultrastructural data.
- ❖ Ecological, floristic investigation of plants in Northern China.
- ❖ Microscopic and ultrastructural study on the anatomy of Staphyleaceae

## GRANT & FELLOWSHIP

- ❖ **Co-PI (2000-2004): DOE Office of Science National Nanotechnology Initiative.** Understanding Nanoscale Chemistry: Quantum Dot Interactions with Proteins and Carbon Nanotubes and the Mediation of Inter-Quantum Dot Communication (PI: Arthur J. Nozik)
- ❖ **PI/co-PI (1991-1997): National Natural Science Foundation of China.**  
PI: Molecular systematics of subtribe Astragalinae (Fabaceae),  
Co-PI: Ancient DNA research (PI: Zhangliang Chen)  
Co-PI: Systematics of Polygonatum (PI: Guangyun Rao)
- ❖ **PI/co-PI (1991-1995): other projects**  
**NLPGE Research Fellowships.** PI: Phylogenetic Reconstruction of Subtribe Astragalinae: Evidence from Restriction Site Mapping of A PCR-amplified Fragment Which Encompassed cpDNA genes *ndhF* and *psbA*.  
**KIB Director Fellowships.** PI: Systematics of Astragalinae

## RECORD OF INVENTION

- ❖ Michael E. Himmel, **Shi-You. Ding**, Garry Rumbles and Arthur J. Nozik Generation of Ordered Arrays of Quantum Dots Using Cellulosome Protein Scaffolds. NREL New Invention No. 01-05.
- ❖ **Shi-You Ding**, William S. Adney, Todd B. Vinzant, Michael E. Himmel A Thermal Tolerant Avicelase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-36, Filed 8/1/01
- ❖ William S. Adney, **Shi-You Ding**, Suzanne McCarter, Michael E. Himmel, Stephen R. Decker, and Todd B. Vinzant. A Thermal Tolerant Exoglucanase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-38, Filed 8/1/01
- ❖ **Shi-You Ding**, William S. Adney, Todd B. Vinzant, Michael E. Himmel. A Thermal Tolerant Multi-Domain Cellulase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-37, Filed 8/1/01
- ❖ **Shi-Y u Ding**, William S. Adney, Todd B. Vinzant, Michael E. Himmel. A Thermal Tolerant Mannanase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-35, Filed 8/1/01

- ❖ Michael E. Himmel, Joshua Sakon, William S. Adney, Stephen R. Decker, Suzanne McCarter, **Shi-You Ding**, Todd B. Vinzant and John O. Baker. Site Specific Mutations Conferring Thermal Tolerance to *Trichoderma reesei* CBHI. NREL New Invention No. 01-31.

## PUBLICATIONS

1. Xu, Q., Gao, W., **Ding, S.-Y.**, Kenig, R., Shoham, Y., Bayer, E. A., Lamed, R. 2003. A cellulosome-integrating gene cluster in *Acetivibrio cellulolyticus* contains a scaffoldin-like gene encoding for a novel type of adaptor protein. *J. Bacteriol.* (in press)
2. **Ding, S.-Y.**, Lamed, R., Bayer, E. A., Himmel, M. E. 2003. The bacterial scaffoldin: structure function and potential applications in the nanosciences. In *Genetic Engineering* (J. K. Setlow, ed.) Volume 25, Kluwer Academic/Plenum Publishers. (in press)
3. **Ding S.-Y.**, William S. Adney, Todd B. Vinzant Stephen R. Decker, John O. Baker, Steven R. Thomas, Michael E. Himmel. Glycosyl Hydrolases Gene Cluster of *Acidothermus cellulolyticus* ACS (in press)
4. Rincon M. T., **Ding, S.-Y.**, Mccrae S. I., Martin J. C., Aurilia V., Lamed R., Shoham Y., Bayer, E. A., Flint, H. J. 2003. Novel organization and divergent dockerin specificities in the cellulosome system of *Ruminococcus flavefaciens*. *J. Bacteriol.* 185:703-713.
5. William S. Adney, Yat-Chen Chou, Stephen R. Decker, **Ding, S.-Y.**, John O. Baker, Todd B. Vinzant, Glenn Kunkel, and Michael E. Himmel. Heterologous Expression of *Trichoderma reesei* 1,4-beta-D-glucan cellobiohydrolase. ACS (in press)
6. **Ding, S.-Y.**, Rincon M. T., Lamed R., Martin J. C., Mccrae S. I., Aurilia V., Shoham Y., Bayer, E. A., Flint, H. J. 2001. Cellulosomal Scaffoldin-Like Proteins from *Ruminococcus flavefaciens*. *J. Bacteriol.* 183:1945-1953.
7. **Ding, S.-Y.** Bayer, E. A., Steriner, D., Shoham, Y. and Lamed, R. 2000. An atypical scaffoldin of the *Bacteroides cellulosolvens* cellulosome that contains eleven type-II cohesins. *J. Bacteriol.* 182:4915-4925
8. Bayer, E. A., **Ding, S.-Y.**, Shoham, Y. and Lamed, R. New perspectives in the structure of cellulosome-related domains from different species. In *Genetics, biochemistry and ecology of cellulose degradation* (K. Ohmiya et al., ed.), 1999. pp. 428-436. Uni Publishers Co., Ltd., Tokyo, Japan.
9. **Ding, S.-Y.**, Bayer, E. A., Steriner, D., Shoham, Y. and Lamed, R. 1999. A Novel Cellulosomal Scaffoldin from *Acetivibrio cellulolyticus* That Contains a Family 9 Glycosyl Hydrolase. *J. Bacteriol.* 181:6720-6729.
10. Bayer, E. A., **Ding, S.-Y.**, Mechaly, A., Shoham, Y. and Lamed, R. 1999. Emerging phylogenetics of cellulosome structure, p. 189-201. In H. Gilbert, G. J. Davies, B. Henrissat, and B. Svensson (eds), *Recent advances in carbohydrate bioengineering*. The Royal Society of Chemistry, Cambridge.
11. **Ding, S.-Y.**, Gu, H., Qu, L., Chen, Z. A preliminary study on the use of RFLP analysis of the PCR amplified products in the systematic investigation of the subtribe Astragalinae (Fabaceae). *Acta Bot. Sin.* 1995, 7-102.
12. **Ding, S.-Y.**, Zhang, C., Gu, H., Chen, Z. Progresses of studies on plant systematics at DNA level. *Acta Bot. Boreal.-Occident. Sin.* 1996,16(3):578-588.
13. **Ding, S.-Y.**, Zhang, C., Gu, H., Chen, Z. General review of the methods of molecular systematics of plants at DNA level. *Acta Bot. Boreal.-Occident. Sin.* 1996,16(2): 197-202.
14. Chu, L., Li, Y., Quan, S., **Ding, S.-Y.**, Suzuki, R., Chen, Z. Sequence analysis and expression in *E. coli* of RDV S7. *Acta Microbiologica Sinica*, 1996,36(5):335-343.
15. **Ding, S.-Y.**, Zhang, C., Gu, H., Chen, Z. Plant systematics at DNA level, in *The Proceeding of the Symposium of the Postdoctor in China*. 1996, Pp. 938-943.
16. Chen, Y., Zhang, C., **Ding, S.-Y.**, Zhang, Z. The taxonomy and analysis of *Artemisia* Linn. In the Loess Plateau of northern Shaanxi. *Acta Bot. Boreal.-Occident. Sin.* 1993,13(3):238-245.
17. **Ding, S.-Y.**, Yu, Z. Systematic signification of leaf structure of Staphyleaceae. *Bull. Bot.* 1992,12(2):177-184.
18. **Ding, S.-Y.**, Yu, Z. The preliminary study on chemical taxonomy of Staphyleaceae. *The 1st Symposium of Systematic Botany in Northwestern China*. 1992,108-111.
19. Zhang, Z., Zhang, C., Chen, Y., **Ding, S.-Y.** A preliminary study in the border line of the floristic regionalization in the Loess Plateau of northern Shaanxi. *Acta Bot. Boreal.-Occident. Sin.* 1992,12(4):303.
20. Zhang, Y., **Ding, S.-Y.** A resource of nectariferous plants in Shaanxi. *Acta Bot. Boreal.-Occident. Sin.* 1991,185-189.
21. **Ding, S.-Y.**, Zhang, Y. The conservation plants in northwestern China, in *Ecological Environment in Northwestern China*. 1991,1:353-364.
22. Zhang, Z., Zhang, C., **Ding, S.-Y.** Plants in the Loess Plateau. In, *The Resource and Application of Plants in the Loess Plateau*. 1991,194-287.
23. **Ding, S.-Y.**, Yu, Z. Study on the pollen of Staphyleaceae. *Acta Bot. Boreal.-Occident. Sin.* 1988,8(5): 29-33.

## Abstracts and presentations in international meetings

1. **Shi-You Ding**, Todd B. Vinzant, William S. Adney, Stephen R. Decker, John O. Baker, Ed Jennings, Michael E. Himmel New Glycosyl Hydrolases from *Acidothermus cellulolyticus* poster for 24<sup>th</sup> Symposium on Biotechnology For Fuels and Chemicals April 28 - May 1, 2002, Gatlinburg, TN
2. **S.-Y. Ding**, WS Adney, SE McCarter, JO Baker, SR Decker, TB Vinzant, ME Himmel. Diversity and Conservation of Relevant Glycoside Hydrolase Families in Well-studied Cellulolytic Microbes. Proctor Academy, Andover, New Hampshire, USA, July 29- Aug.3, 2001.
3. Marco Rincón, **Shi-You Ding**, Sheila McCrae, Jennifer Martin, Ed Bayer, Raphael Lamed, Yuval Shoham, Vincenzo Aurilia, and Harry Flint. Cellulosomal proteins assembly in rumen cellulolytic bacterium *Ruminococcus flavefaciens*. Proctor Academy, Andover, New Hampshire, USA, July 29- Aug.3, 2001.
4. **Ding, S.-Y.** cellulosomes in *Acetivibrio cellulolyticus* and *Bacteroides cellulosolvens*. Gordon Research Conference on Cellulases and Cellulosomes, Proctor Academy, Andover, New Hampshire, USA, July 25-30, 1999. (Oral presentation)

5. **Ding, S-Y.**, Bayer, E. A., Shoham, Y. and Lamed, R., McCrae, S. I., Kirby, J., Aurilia, V., and Flint, H. J. Preliminary evidence of high-molecular-weight scaffoldin-like proteins from *Ruminococcus flavefaciens*. 3<sup>rd</sup> Carbohydrate Bioengineering Meeting, University of Newcastle Upon Tyne, UK, 11<sup>th</sup>-14<sup>th</sup> April 1999. P5.12
6. **Ding, S-Y.**, Steiner, D., Kenig, R., Yaron, S., Morag, E., Shoham, Y., Bayer, E., Lamed, R. Evidence for cohesin and CBD domains, characteristic of cellulosomes in non-clostridial anaerobic bacteria. 8<sup>th</sup> International Symposium on the Genetics of Industrial Microorganisms, Jerusalem, Israel, June 28-July 2, 1998. p50.
7. **Ding, S-Y.**, Steiner, D., Kenig, R., Yaron, S., Morag, E., Shoham, Y., Bayer, E., Lamed, R. Domain organization and sequence of the first non-clostridial scaffoldin from *Acetivibrio cellulolyticus*. Mie Bioforum, Genetics, biochemistry and ecology of cellulose degradation, Suzuka, Japan, Sept. 7-11, 1998. p47.
8. **Ding, S-Y.**, Steiner, D Kenig, R Yaron, S., Morag, E Shoham, Y Bayer, E Lamed, R. Unique Cellulosome-related protein in *Bacteroides cellulosovens*. Mie Bioforum 98, Genetics, biochemistry and ecology of cellulose degradation, Suzuka, Japan, Sept. 7-11, 1998. p49.

# CAZy - Carbohydrate-Active enZymes

Home Access by Family Access by Organism Acknowledgements Links Team CitingCAZy Search

Family GH5

Family GH5

**CAZy Family** Glycoside Hydrolase Family 5

**Known Activities** Endoglycosylceramidase (EC 3.2.1.123);  $\beta$ -mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1.4); Glucan 1,3- $\beta$ -glucosidase (EC 3.2.1.58); Licheninase (EC 3.2.1.73); Glucan endo-1,6- $\beta$ -glucosidase (EC 3.2.1.75); Mannan endo-1,4- $\beta$ -mannosidase (EC 3.2.1.78); Endo-1,4- $\beta$ -xylanase (EC 3.2.1.8); Cellulose 1,4- $\beta$ -cellobiosidase (EC 3.2.1.91).

**Mechanism** Retaining

**Catalytic Nucleophile/Base** Glu (experimental)

**Catalytic Proton Donor** Glu (experimental)

**3D Structure Status** Available (see PDB). Fold ( $\beta/\alpha$ )<sub>8</sub>

**Clan** GH-A

**Note** formerly known as cellulase family A.

**Relevant Links** HOMSTRAD; InterPro; PFAM; PROSITE

**Statistics** CAZy(363); GenBank/GenPept (487); Swissprot (177); PDB (43); 3D(13); cryst(1)

Protein	Organism	EC#	GenBank / GenPept	SwissProt PDB / 3D
endo-1,4-glucanase	<i>Acidothermus cellulolyticus</i>	3.2.1.4	U33212 AAA75477.1 AX467594 CAD42489.1	<b>P54583</b> 1C0D A 1ECE A
endo-1,4-glucanase	<i>Actinomyces sp. 40</i>	3.2.1.4	U94825 AAC06196.1	<b>O66064</b>
xylanase	<i>Aeromonas caviae</i>	3.2.1.8	D88553 BAA13641.1	<b>P70733</b>
xylanase D	<i>Aeromonas caviae</i>	3.2.1.8	U86340 AAB63573.1	<b>O24852</b>
$\beta$ -mannanase	<i>Agaricus bisporus</i>	3.2.1.78	Z50095 CAA90423.1	<b>Q92401</b>
exo-1,3-glucanase 1	<i>Agaricus bisporus</i>	3.2.1.58	X92961 CAA63536.1	<b>Q12539</b>
mannanase (Cel4A)	<i>Agaricus bisporus C54-carb8</i>	3.2.1.78	AJ271862 <b>CAB76904.1</b>	Q9P893
exo-1,3-glucanase 2 (fragment)	<i>Agaricus bisporus Horst U1</i>	3.2.1.58	X92961 CAA63537.1	<b>Q12540</b>
ORF PCZA361.14	<i>Amycolatopsis orientalis</i>	n.d.	AJ223998 CAA11771.1	<b>O52801</b>
endo-1,4-glucanase CelB	<i>Anaerocellum thermophilum</i>	3.2.1.4	Z86104 CAB06784.1	<b>P96310</b>
endo-1,4-glucanase CelD	<i>Anaerocellum thermophilum</i>	3.2.1.4	Z77855 CAB01405.1	<b>Q59154</b>
ORF At1g02310/T6A9.1	<i>Arabidopsis thaliana</i>	n.d.	AC064879 AAG00883.1 AY081352 AAL91241.1 BT002154 AAN72165.1 NC_003070 NP_171733.1	Q9FZ29

B



ORF At1g13130/F3F19.15	<i>Arabidopsis thaliana</i>	n.d.	AC007357 <b>AAD31066.1</b> NM_101183 NP_172772.1		
ORF At2g20680	<i>Arabidopsis thaliana</i>	n.d.	AC006234 <b>AAD20927.1</b>	<b>Q9SKU9</b>	
ORF At3g10890/T7M13.3	<i>Arabidopsis thaliana</i>	n.d.	AC011708 <b>AAF19560.1</b> NM_111926 NP_187700.1	<b>Q9SG94</b>	
ORF At3g10900/T7M13.2	<i>Arabidopsis thaliana</i>	n.d.	AC011708 <b>AAF19559.1</b> NM_111927 NP_187701.1	<b>Q9SG95</b>	
ORF At3g26130/MTC11.2	<i>Arabidopsis thaliana</i>	n.d.	AB024038 <b>BAB02432.1</b> NC_003074 NP_189244.1	<b>Q9LTN0</b>	
ORF At3g26140/MTC11.4	<i>Arabidopsis thaliana</i>	n.d.	AB024038 <b>BAB02434.1</b> NC_003074 NP_189245.1	<b>Q9LTM8</b>	
ORF At3g30540/MQP15.4	<i>Arabidopsis thaliana</i>	n.d.	AB016878 <b>BAB01021.1</b> NC_003074 NP_189675.1	<b>Q9LW44</b>	
ORF At4g28320	<i>Arabidopsis thaliana</i>	n.d.	AL161572 <b>CAB79634.1</b> NM_118972 NP_194561.1	<b>Q9M0H6</b>	
ORF At5g01930/T20L15_200	<i>Arabidopsis thaliana</i>	n.d.	BT005831 <b>AAO64766.1</b> AL162351 <b>CAB82763.1</b> NM_120271 NP_195813.1	<b>Q9LZV3</b>	
ORF At5g16700/F5E19_40	<i>Arabidopsis thaliana</i>	n.d.	AL391147 <b>CAC01834.1</b> NM_121675 NP_197172.1		
ORF At5g17500/K3M16_70	<i>Arabidopsis thaliana</i>	n.d.	AL391150 <b>CAC01894.1</b> NM_121756 NP_197252.1		
ORF At5g66460/K1F13.12	<i>Arabidopsis thaliana</i>	n.d.	BT000452 <b>AAN17429.1</b> AB013389 <b>BAB10922.1</b> NM_126044 NP_201447.1	<b>Q9FJZ3</b>	
$\beta$ -mannanase	<i>Aspergillus aculeatus</i>	3.2.1.78	L35487 <b>AAA67426.1</b>	<b>Q00012</b>	
endoglucanase II	<i>Aspergillus aculeatus</i>	n.d.	AF543446 <b>AAN16396.1</b> AY173077 <b>AAN75019.1</b>		
FII-CMCase	<i>Aspergillus aculeatus</i>	3.2.1.4	AB015510 <b>BAA29030.1</b>	<b>O74169</b>	
endo-1,4-glucanase V	<i>Aspergillus aculeatus</i> WO 94/14953	3.2.1.4	AF054512 <b>AAC08587.1</b>	<b>O59951</b>	
endoglucanase A (EglA)	<i>Aspergillus kawachii</i>	n.d.	AB055431 <b>BAB62317.1</b>		
endoglucanase C (EglC)	<i>Aspergillus kawachii</i>	n.d.	AB055433 <b>BAB62319.1</b>		
endo-1,4-glucanase B (EglB)	<i>Aspergillus niger</i> CBS 120.49	3.2.1.4	AJ224452 <b>AAE60102.1</b> <b>AAE84292.1</b> <b>CAA11965.1</b>	<b>O74706</b>	
endoglucanase (Eng1)	<i>Aspergillus niger</i> IFO31125	3.2.1.4	AF331518 <b>AAG50051.1</b>		
unnamed protein product	<i>Aspergillus oryzae</i>	n.d.	AX011537 <b>CAC07551.1</b>		
ORF egl	<i>Azorhizobium</i> <i>caulinodans</i> ORS571	n.d.	Z48958 -		
endo-1,4-glucanase Cel5A	<i>Cel5A</i> <i>Bacillus agaradherans</i>	3.2.1.4	AF067428 <b>AAC19169.1</b>	<b>O85465</b>	1A3H _ 1E5J A 1H11 A 1H2J A 1H5V A 1HF5 A 1HF6 A 1HF7 A 1OCQ 1QHZ A 1QI0 A 1QI2 A 2A3H _ 3A3H _ 4A3H A 5A3H A 6A3H A 7A3H A 8A3H A
endoglucanase A (EngA)	<i>Bacillus</i> <i>amyloliquefaciens</i>	n.d.	AF363635 <b>AAL99668.1</b>		

<b>UMAS1002</b>					
$\beta$ -mannanase	<i>Bacillus circulans</i> K-1	3.2.1.78	AB007123 BAA25878.1	<b>O66185</b>	
ORF BH0603	<i>Bacillus halodurans</i> C-125	n.d.	AP001509 BAB04322.1 NC_002570 NP_241469.1	<b>Q9KF82</b>	
endo-1,4-glucanase 3a	<i>Bacillus lautus</i>	3.2.1.4	A28175 <b>CAA01935.1</b>		
endo-1,4-glucanase B	<i>Bacillus lautus</i>	3.2.1.4	M33762 AAA22408.1 A28172 CAA01934.1	<b>P23550</b>	
endo-1,4-glucanase	<i>Bacillus polymyxa</i>	3.2.1.4	M33791 AAA22631.1	<b>P23548</b>	
unnamed protein product	<i>Bacillus</i> sp.	n.d.	- <b>AAE86309.1</b> AX665431 CAD82874.1		
unnamed protein product	<i>Bacillus</i> sp.	n.d.	AX643592 <b>CAD67813.1</b>		
endo-1,4-glucanase	<i>Bacillus</i> sp. 1139	3.2.1.4	M15743 AAA22305.1 D00066 BAA00045.1	<b>P06564</b>	
endo-1,4-glucanase	<i>Bacillus</i> sp. 22-28	3.2.1.4	D85236 BAA12744.1	<b>Q45554</b>	
endo-1,4-glucanase	<i>Bacillus</i> sp. 5H	3.2.1.4	AB016164 BAA31712.1	<b>O83012</b>	
CelS	<i>Bacillus</i> sp. 79-23	3.2.1.4	AF045482 AAC02536.1	<b>O52731</b>	
endo-1,4-glucanase A	<i>Bacillus</i> sp. BP-23	3.2.1.4	Y12512 CAA73113.1	<b>O08342</b>	
cellulase	<i>Bacillus</i> sp. CBS 670.93	3.2.1.4	A76937 CAB58698.1 A79880 <b>CAB59165.1</b> AX665429 CAD82873.1		1LF1 A
endo-1,4-glucanase	<i>Bacillus</i> sp. D04	3.2.1.4	U27084 AAC43478.1	<b>Q45430</b>	
endo-1,4-glucanase	<i>Bacillus</i> sp. KSM-635	3.2.1.4	M27420 AAA22304.1	<b>P19424</b>	1G01 A 1G0C A
endo-1,4-glucanase	<i>Bacillus</i> sp. KSM-64	3.2.1.4	M84963 AAA73189.1	<b>Q59241</b>	
endoglucanase N252 (Egl252)	<i>Bacillus</i> sp. KSM-N252	3.2.1.4	AB057671 <b>BAB62295.1</b>		
cellulase	<i>Bacillus</i> sp. KSM-S237	3.2.1.4	AB018420 <b>BAB19360.1</b>		
endo-1,4-glucanase A	<i>Bacillus</i> sp. N-4	3.2.1.4	M14781 AAA22301.1	<b>P06566</b>	
endo-1,4-glucanase B	<i>Bacillus</i> sp. N-4	3.2.1.4	M14729 AAA22299.1	<b>P06565</b>	
endo-1,4-glucanase C	<i>Bacillus</i> sp. N-4	3.2.1.4	M25500 AAA22306.1	<b>P19570</b>	
endo-1,4-glucanase B1	<i>Bacillus</i> sp. N186-1	3.2.1.4	Z33876 CAA83942.1	<b>Q59232</b>	
cellulase (CelA)	<i>Bacillus</i> sp. NBL420	n.d.	AY039744 <b>AAK73277.1</b>		
endo-1,4-glucanase	<i>Bacillus subtilis</i>	3.2.1.4	M28332 AAA22307.1	<b>Q45532</b>	
endo-1,4-glucanase	<i>Bacillus subtilis</i> BSE616	3.2.1.4	D01057 BAA00859.1	<b>P23549</b>	
endo-1,4- $\beta$ -glucanase	<i>Bacillus subtilis</i> CHZ1	3.2.1.4	AY044252 <b>AAK94871.1</b>		
endo-1,4-glucanase	<i>Bacillus subtilis</i> DLG	3.2.1.4	M16185 AAA22496.1	<b>P07983</b>	
endo-1,4-glucanase (EglS or BglC)	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	3.2.1.4	AF355629 AAK39540.1 X04689 CAA28392.1 X67044 CAA47429.1 Z29076 CAA82317.1 Z73234 CAA97610.1 Z99113 CAB13696.1 NC_000964 NP_389695.1	<b>P10475</b>	
ORF YnfF	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	n.d.	Z73234 CAA97612.1 Z99113 CAB13698.1	<b>Q45070</b>	
endo-1,4-glucanase	<i>Bacteroides rumenicola</i>	3.2.1.4	M38216 AAA22909.1	<b>Q44878</b>	
BT3043	<i>Bacteroides thetaiotaomicron</i> VPI-5482	n.d.	AE016938 <b>AAO78149.1</b> NC_004663 NP_811955.1		
BL0157	<i>Bifidobacterium longum</i> NCC2705	n.d.	AE014632 <b>AAN24012.1</b> NC_004307 NP_695376.1		
BL1333	<i>Bifidobacterium longum</i> NCC2705	n.d.	AE014762 <b>AAN25133.1</b> NC_004307 NP_696497.1		
BL1761	<i>Bifidobacterium longum</i> NCC2705	n.d.	AE014810 <b>AAN25544.1</b> NC_004307 NP_696908.1		
$\beta$ -1,3-glucanase	<i>Blumeria graminis</i>	3.2.1.-	AF317734 <b>AAL26905.1</b>		
blr3367	<i>Bradyrhizobium japonicum</i> USDA110	n.d.	AP005947 BAC48632.1 NC_004463 NP_770007.1		

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endo-1,4-glucanase A		<i>Butyrivibrio fibrisolvens</i> A46	3.2.1.4	M37031 AAA20893.1	P22541	
endo-1,4-glucanase 1		<i>Butyrivibrio fibrisolvens</i> H17c	3.2.1.4	X17538 CAA35574.1	P20847	
$\beta$ -1,4-mannanase (ManA)		<i>Caldibacillus cellulovorans</i>	3.2.1.78	AF163837 <b>AAF22274.1</b>	Q9RFX5	
$\beta$ -mannanase/endo-1,4-glucanase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.4 3.2.1.78	L01257 AAA71887.1 M36063 AAA72861.1	P22533	
endo-1,4-glucanase/cellobiohydrolase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.91 3.2.1.4	X13602 CAA31936.1	P10474	
CelB (multidomain protein)		<i>Caldicellulosiruptor</i> sp. Tok7B.1	n.d.	AF078737 <b>AAD30364.1</b>	Q9X3P6	
exo-1,3-glucanase		<i>Candida albicans</i>	3.2.1.58	X56556 CAA39908.1	P29717	1CZ1 A 1EQC A 1EQP A
1,3- $\beta$ -glucanase (EXG1)		<i>Candida oleophila</i>	n.d.	AF393806 <b>AAM21469.1</b>		
ORF CC0801		<i>Caulobacter crescentus</i> CB15	n.d.	AE005756 <b>AAK22786.1</b> NC_002696 NP_419618.1	Q9AA10	
endo-1,4-glucanase D	Cel5A	<i>Cellulomonas fimi</i>	3.2.1.4	L02544 AAA23089.1	P50400	
endo-1,4-glucanase B (cflB)		<i>Cellulomonas flavigena</i>	3.2.1.4	AF172345 <b>AAD48494.2</b>		
endo-b1,4-mannanase 5A	Man5A	<i>Cellvibrio japonicus</i>	n.d.	AY187031 <b>AAO31759.1</b>		
endo-b1,4-mannanase 5B	Man5B	<i>Cellvibrio japonicus</i>	n.d.	AY187032 <b>AAO31760.1</b>		
endo-b1,4-mannanase 5C	Man5C	<i>Cellvibrio japonicus</i>	n.d.	AY187033 <b>AAO31761.1</b>		
cellodextrinase C		<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )	3.2.1.-	X61299 CAA43597.1	P27033	
endo-1,4-glucanase E		<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )	3.2.1.4	X86798 CAA60493.1	Q59665	
endo-1,4-glucanase A		<i>Cellvibrio mixtus</i>	3.2.1.4	AF003696 AAB61461.1	O07652	
endo-1,4-glucanase B		<i>Cellvibrio mixtus</i>	3.2.1.4	AF003697 <b>AAB61462.2</b>	O07653	
ORF manB (fragment)		<i>Chlorella vulgaris</i> C-169	n.d.	AB036816 <b>BAA99563.1</b>		
Cellulase CelA		<i>Clavibacter michiganensis</i> NCPPB 382	3.2.1.4	X62582 <b>CAA44467.2</b>	Q9K5C7	
cellulase CelA		<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>	3.2.1.4	AY007311 <b>AAK16222.1</b>	Q9AF65	
endo-1,4-glucanase C307		<i>Clostridium</i> sp. F1	3.2.1.4	D00945 BAA00793.1	P23340	
endo-1,4-glucanase		<i>Clostridium acetobutylicum</i>	3.2.1.4	M31311 AAA23230.1	P15704	
ORF CAC0706		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007585 <b>AAK78683.1</b>	Q97L56	
ORF CAC0825		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007598 <b>AAK78801.1</b>	Q97KU1	
ORF CAC0826		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007598 <b>AAK78802.1</b>	Q97KU0	
ORF CAC0912		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007607 <b>AAK78888.1</b>	Q97KK6	
ORF CAC0918		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007607 <b>AAK78894.1</b>	Q97KK1	
ORF CAC3469		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007844 <b>AAK81397.1</b>	Q97DK6	
ORF CAP0118		<i>Clostridium</i>	n.d.	AE001438 AAK76863.1	Q97TI3	

		<i>ac. tobutylicum</i> ATCC 824		NC_001988 NP_149281.1	
ORF CAP0119		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE001438 AAK76864.1 NC_001988 NP_149282.1	Q97TI2
$\beta$ -1,4-glucanase (Cel5I)	Cel5I	<i>Clostridium cellulolyticum</i>	n.d.	AY077754 AAL79562.1	
cellulase CelIN		<i>Clostridium cellulolyticum</i>	3.2.1.4	AF316823 AAG45162.1	Q9EYQ0
endo-1,4-glucanase A		<i>Clostridium cellulolyticum</i>	3.2.1.4	M32362 AAA23221.1 M93096 AAA51444.1	P17901 1EDG _
endo-1,4-glucanase D		<i>Clostridium cellulolyticum</i>	3.2.1.4	D90341 BAA14354.1	P25472
mannanase ManK		<i>Clostridium cellulolyticum</i>	3.2.1.78	AF316823 AAG45159.1	Q9EYQ3
endo-1,4-glucanase 5A (EngF)	Cel5A	<i>Clostridium cellulovorans</i>	3.2.1.4	U37056 AAB40891.1	P94622 3D
endo-1,4-glucanase B		<i>Clostridium cellulovorans</i>	3.2.1.4 3.2.1.8 3.2.1.73	M75706 AAA23231.1	P28621
endo-1,4-glucanase D		<i>Clostridium cellulovorans</i>	3.2.1.4	M37434 AAA23233.1	P28623
endo-1,4-glucanase E (EngE)		<i>Clostridium cellulovorans</i>	3.2.1.4	AF105331 AAD39739.1	Q9XD99
mannanase A (ManA)		<i>Clostridium cellulovorans</i>	3.2.1.78	AF132735 AAF06110.2	
endo-1,4-glucanase A		<i>Clostridium josui</i>	3.2.1.4	D85526 BAA12826.1	Q59290
endo-1,4-glucanase (CelA)		<i>Clostridium longisporum</i>	3.2.1.4	L02868 AAC37035.1	P54937
endo-1,4-glucanase E	Cel5C	<i>Clostridium thermocellum</i>	3.2.1.4	M22759 AAA23224.1	P10477
1,4- $\beta$ -cellobiohydrolase (CelO)		<i>Clostridium thermocellum</i> F7	3.2.1.91	AJ275975 CAB76938.1	
endo-1,4-glucanase C (CelC)		<i>Clostridium thermocellum</i> F7	3.2.1.4	AJ307315 CAC27410.1	
endo-1,4-glucanase B	Cel5A	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	X03592 CAA27266.1	P04956
endo-1,4-glucanase C	Cel5B	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	M19422 AAA23220.1	P07985 1CEC _ 1CEN _ 1CEO _
endo-1,4-glucanase G	Cel5D	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	X69390 CAA49187.1	Q05332
endo-1,4-glucanase H (CelH)	Cel26A-Cel5E	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	M31903 AAA23225.1	P16218
exo-1,3- $\beta$ -glucanase		<i>Cochliobolus carbonum</i>	3.2.1.58	AF229446 AAF65310.1	
endo-1,4-glucanase 1		<i>Cryptococcus flavus</i>	3.2.1.4	S45137 AAC60541.1 D13967 BAA03070.1	Q04469
exo- $\beta$ -1,3-glucanase (fragment)		<i>Cryptococcus neoformans</i> var. <i>neoformans</i>	n.d.	AF243533 AAM26269.1	
endo- $\beta$ -mannanase (fragment)		<i>Datura ferox</i>	n.d.	AF323949 AAO06964.1	
exo-1,3-glucanase		<i>Debaryomyces occidentalis</i> ( <i>S. occidentalis</i> )	3.2.1.58	Z46871 CAA86951.1	Q12700
endo-1,4-glucanase A (eglA)		<i>Emericella nidulans</i>	3.2.1.4	AB009402 BAA82592.1	
cellulase CelA		<i>Epidinium caudatum</i>	n.d.	AB104618 BAC57895.1	

endo-1,4-glucanase	<i>Epidinium caudatum</i>	3.2.1.4	AB011273 <b>BAA76394.1</b>	
endoglucanase Epi2	<i>Epidinium caudatum</i>	n.d.	AB104616 <b>BAC57893.1</b>	
endo-1,4-glucanase N	<i>Erwinia carotovora atroseptica</i>	3.2.1.4	L39788 AAC37033.1	<b>Q59394</b>
endo-1,4-glucanase V1	<i>Erwinia carotovora</i> SCC3193	3.2.1.4	X79241 CAA55823.1	<b>Q59395</b>
endo-1,4-glucanase V	<i>Erwinia carotovora</i> SCRI193	3.2.1.4	X76000 CAA53592.1	<b>Q47096</b>
endo-1,4-glucanase CelA (fragment)	<i>Erwinia carotovora</i> subsp. <i>carotovora</i> LY34	3.2.1.4	AF025768 AAC02964.1	<b>O31029</b>
xylanase	<i>Erwinia chrysanthemi</i>	3.2.1.8	U41750 AAB53151.1	<b>Q46961</b> 1NOF
endo-1,4-glucanase Z	<i>Cel5A</i> <i>Erwinia chrysanthemi</i> 3937	3.2.1.4	Y00540 CAA68604.1	<b>P07103</b> 1EGZ A
endo-1,4-glucanase 3	<i>Fibrobacter intestinalis</i>	3.2.1.4	L39840 AAA92982.1	<b>Q59440</b>
endo-1,4-glucanase 3	<i>Fibrobacter succinogenes</i>	3.2.1.4	M29047 AAA24893.1	<b>P14250</b>
endo-1,4-glucanase G	<i>Fibrobacter succinogenes</i>	3.2.1.4	U33887 AAB38548.1	<b>Q47916</b>
cellodextrinase A (CedA)	<i>Fibrobacter succinogenes</i> S85	3.2.1.-	U07419 AAA50210.1	<b>Q59441</b>
CMC-xylanase (fragment)	<i>Fibrobacter succinogenes</i> S85	3.2.1.4	U94826 AAC06197.1	<b>O66065</b>
cellulase (Celc)	<i>Filobasidiella neoformans</i> 309 Cap67	n.d.	AJ486863 <b>CAD31110.1</b>	
$\beta$ -mannanase	<i>Geobacillus stearothermophilus</i> MCA2184	3.2.1.78	AF038547 <b>AAC71692.1</b>	
endoglucanase 1 (Eng1)	<i>Globodera rostochiensis</i>	3.2.1.4	AF004523 AAC48325.1 AF056110 AAC63988.1	<b>O16028</b>
endoglucanase 2 (Eng2)	<i>Globodera rostochiensis</i>	3.2.1.4	AF004716 AAC48341.1 AF056111 AAC63989.1	<b>O44078</b>
$\beta$ -1,4-endoglucanase precursor (Eng-3)	<i>Globodera rostochiensis</i> Ro-1 Mierenbos	3.2.1.4	AF408154 <b>AAN03645.1</b> AF408155 AAN03646.1	
$\beta$ -1,4-endoglucanase precursor (Eng-4)	<i>Globodera rostochiensis</i> Ro-1 Mierenbos	3.2.1.4	AF408156 <b>AAN03647.1</b> AF408157 AAN03648.1	
endoglucanase 1 (Eng1)	<i>Heterodera glycines</i>	3.2.1.4	AF052733 AAC15707.1 AF006052 AAC48327.1 A79341 CAB59144.1	<b>O18453</b>
endoglucanase 2 (Eng2)	<i>Heterodera glycines</i>	3.2.1.4	AF006053 AAC48326.1 A79340 CAB59143.1	<b>O18454</b>
endoglucanase 3	<i>Heterodera glycines</i>	3.2.1.4	AF044210 AAC33848.1 AF056048 AAC33860.1	<b>O77449</b>
endoglucanase 4	<i>Heterodera glycines</i>	3.2.1.4	AY043224 <b>AAK85303.1</b>	
endo-1,4-glucanase	<i>Humicola grisea</i>	3.2.1.4	D84470 BAA12676.1	<b>Q12620</b>
endo-1,4-glucanase IV	<i>Humicola insolens</i>	3.2.1.4	X76046 CAA53631.1	<b>Q12624</b>
$\beta$ -1,6-glucanase precursor (Bgn3)	<i>Hypocrea virens</i>	n.d.	AF395757 <b>AAL84696.1</b>	
exo-1,3-glucanase	<i>Kluyveromyces lactis</i>	3.2.1.58	Z46869 CAA86949.1	<b>Q12628</b>
mannanase (Lm1)	<i>Lactuca sativa</i>	n.d.	AJ315978 CAC51690.1 AJ315978 <b>CAC51690.2</b>	<b>Q93X40</b>
Xyl38	<i>Leptosphaeria maculans</i>	n.d.	AF487263 <b>AAO49459.1</b>	
LB251	<i>Leptospira interrogans</i> serovar <i>lai</i> str. 56601	n.d.	AE011612 <b>AAN51810.1</b> NC_004343 NP_714795.1	
$\beta$ -1,4-mannanase (Man2)	<i>Lycopersicon esculentum</i>	3.2.1.78	AF184238 <b>AAG00315.1</b>	
$\beta$ -mannanase	<i>Lycopersicon esculentum</i>	3.2.1.78	AF017144 AAB87859.1	<b>O48540</b>
endo- $\beta$ -mannanase	<i>Lycopersicon esculentum</i>	3.2.1.78	AY034075 AAK56557.1 AY046589 AAK97759.2	

endo-1,4-glucanase 1	<i>Macrophomina phaseolina</i>	3.2.1.4	AY046588 <b>AAK97760.1</b> U14948 AAB51451.1	<b>Q12638</b>	
endo-1,4-glucanase 2	<i>Macrophomina phaseolina</i>	3.2.1.4	U13914 AAB03889.1	<b>Q12637</b>	
$\beta$ -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne arenaria</i>	3.2.1.4	AF323097 <b>AAK21892.1</b>		
$\beta$ -1,4-endoglucanase Eng-1ii (fragment)	<i>Meloidogyne arenaria</i>	3.2.1.4	AF323098 <b>AAK21893.1</b>		
$\beta$ -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne hapla</i>	3.2.1.4	AF323096 <b>AAK21891.1</b>		
$\beta$ -1,4-endoglucanase Eng-1a	<i>Meloidogyne incognita</i>	3.2.1.4	AF323087 <b>AAK21882.1</b>	<b>Q9BJZ1</b>	
$\beta$ -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323090.1 <b>AAK21885.1</b>		
$\beta$ -1,4-endoglucanase Eng-1ii (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323091 <b>AAK21886.1</b>		
$\beta$ -1,4-endoglucanase Eng-1iii (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323092 <b>AAK21887.1</b>		
$\beta$ -1,4-endoglucanase Eng-1iv (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323093 <b>AAK21888.1</b>		
$\beta$ -1,4-endoglucanase Eng-1v (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323094 <b>AAK21889.1</b>		
$\beta$ -1,4-endoglucanase Eng-1vi (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323095 <b>AAK21890.1</b>		
$\beta$ -1,4-endoglucanase Eng-2 (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323086 <b>AAK21881.1</b>		
$\beta$ -1,4-endoglucanase Eng-2a	<i>Meloidogyne incognita</i>	3.2.1.4	AF323088 <b>AAK21883.2</b>		
$\beta$ -1,4-endoglucanase Eng-2b (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323089.1 <b>AAK21884.1</b>		
endo-1,4-glucanase 1 (Eng-1)	<i>Meloidogyne incognita</i>	3.2.1.4	AF100549 <b>AAD45868.1</b>	<b>Q9UA57</b>	
xylanase (Xyl-1)	<i>Meloidogyne incognita</i>	3.2.1.8	AF224342 <b>AAF37276.1</b>		
$\beta$ -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne javanica</i>	3.2.1.4	AF323099 <b>AAK21894.1</b>		
$\beta$ -1,4-endoglucanase Eng-1ii (fragment)	<i>Meloidogyne javanica</i>	3.2.1.4	AF323100 <b>AAK21895.1</b>		
Mr2086	<i>Mesorhizobium loti</i> MAFF303099	n.d.	NC_002678 <b>NP_103519.1</b>		
Mr3893	<i>Mesorhizobium loti</i> MAFF303099	n.d.	NC_002678 <b>NP_104903.1</b>		
endo-1,4-mannanase	<i>Mytilus edulis</i>	3.2.1.78	AJ271365 <b>CAC81056.1</b>		cryst
endo-1,4-glucanase A	<i>Neocallimastix frontalis</i>	3.2.1.4	U38843 AAC63094.1	<b>Q01409</b>	
endo-1,4-glucanase B (CelB)	<i>Neocallimastix patriciarum</i>	3.2.1.4	X77186 AAE59927.1 Z31364 CAA83238.1 CAA83238.1	<b>Q12647</b>	
endo-1,4-glucanase D (CelD)	<i>Neocallimastix patriciarum</i>	3.2.1.4	AF053363 AAC06321.1	<b>O59943</b>	
$\beta$ -1,6-glucanase	<i>Neotyphodium</i> sp. FFCB_2002	3.2.1.75	AF535131 <b>AAN04103.1</b>		
ORF B23L21.220	<i>Neurospora crassa</i>	n.d.	AL356172 <b>CAB91690.1</b>		
ORF Alr0290	<i>Nostoc</i> sp. PCC 7120	n.d.	AP003581 BAB77814.1 NC_003272 <b>NP_484334.1</b>		
endo-1,4-glucanase	<i>Orpinomyces joyonii</i>	3.2.1.4	U59432 AAC49731.1	<b>P87211</b>	
endo-1,4-glucanase CelB	<i>Orpinomyces joyonii</i>	3.2.1.4	AF015249 AAB69348.1	<b>O13334</b>	
endo-1,4-glucanase CelB29	<i>Orpinomyces joyonii</i>	3.2.1.4	AF015248 AAB69347.1	<b>O13333</b>	

endo-1,4-glucanase B	<i>Orpinomyces</i> sp. PC-2	3.2.1.4	U57818 AAD04193.1 AAE59925.1	<b>P78719</b>
mannanase ManA	<i>Orpinomyces</i> sp. PC-2	n.d.	AF177206 <b>AAL01213.1</b>	
OJ1208D02.11	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AC107314 <b>AAM08620.1</b>	
OJ1208D02.5 or OJ1003C07.1	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AC107314 <b>AAM08614.1</b> AC113335 <b>AAM08821.1</b>	
OSJNBa0010E04.2	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AC096687 <b>AAL79758.1</b>	
OSJNBa0010E04.20	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AC096687 <b>AAL79761.1</b>	
OSJNBb0011N17.6	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AL606614 <b>CAD41089.1</b>	
OSJNBb0011N17.7	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AL606614 <b>CAD41090.1</b>	
OSJNBb0011N17.8	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AL606614 <b>CAD41091.1</b>	
P0481E12.1	<i>Oryza sativa</i>	n.d.	AP003076 <b>BAB56016.1</b>	
(OSJNBa0014K08.29)	( <i>japonica</i> cultivar-group)	n.d.	AP003376 <b>BAC05600.1</b>	
P0671D01.24	<i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)	n.d.	AP003284 <b>BAB91747.1</b>	
endo- $\beta$ -1,4-glucanase	<i>Paenibacillus</i> sp. KCTC8848P	n.d.	AF345984 <b>AAL83749.1</b>	
43 kDa glycoprotein	<i>Paracoccidioides</i> <i>brasiliensis</i> B339	n.d.	U26160 AAC49253.1	<b>Q01575</b>
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41620 (=Pb-9)	n.d.	AB047690 <b>BAB12190.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41621 (=Pb-18)	n.d.	AB047691 <b>BAB12191.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41624 (=Bt-4)	n.d.	AB047693 <b>BAB12193.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41626 (=Bt-9)	n.d.	AB047694 <b>BAB12194.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41632	n.d.	AB047695 <b>BAB12195.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46215	n.d.	AB047696 <b>BAB12196.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46463 (=Tatu)	n.d.	AB047700 <b>BAB12200.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46465 (=Pb-267)	n.d.	AB047692 <b>BAB12192.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46467	n.d.	AB047699 <b>BAB12199.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46468(P-25)	n.d.	AB047698 <b>BAB12198.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46930	n.d.	AB047697 <b>BAB12197.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM47183 (=PRT1-Tatu 1)	n.d.	AB047701 <b>BAB12201.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM47185 (=PRT2 Y)	n.d.	AB047702 <b>BAB12202.1</b>	
43 kDa glycoprotein (Gp43)	<i>Paracoccidioides</i>	n.d.	AB047704 <b>BAB12204.1</b>	

(fragment)	<i>brasiliensis IFM47217</i> (=D4S1=Tatu 4)			
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides brasiliensis IFM47217</i> (=D4S9)	n.d.	AB047703 <b>BAB12203.1</b>	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides brasiliensis IFM47247</i> (=D4LIV1)	n.d.	AB047705 <b>BAB12205.1</b>	
endo-xylanase (XynA)	<i>Pectobacterium chrysanthemi P860219</i>	n.d.	AY055730 <b>AAL16415.1</b>	
endo-1,4-glucanase II	<i>Penicillium janthinellum</i>	3.2.1.4	X89564 CAA61740.1	<b>Q12665</b>
ORF Exo1	<i>Phytophthora infestans</i>	n.d.	AF494014 <b>AAM18483.1</b>	
ORF Exo2	<i>Phytophthora infestans</i>	n.d.	AF494016 <b>AAM18485.1</b>	
ORF Exo3	<i>Phytophthora infestans</i>	n.d.	AF494015 <b>AAM18484.1</b>	
exo-1,3-glucanase	<i>Pichia angusta</i>	3.2.1.58	Z46868 CAA86948.1	<b>Q12626</b>
exo-1,3-glucanase	<i>Pichia anomala K</i>	3.2.1.58	AJ222862 CAA11018.1	<b>O83983</b>
endoglucanase 5A	<i>Cel5A Piromyces equi</i>	3.2.1.4	AJ277483 <b>CAB92326.1</b>	
endoglucanase (egl-1)	<i>Piromyces rhizinflata</i>	3.2.1.4	AF165266 AAD43818.1	<b>Q9Y870</b>
cellulase CelA (fragment)	<i>Polyplastron multivesiculatum</i>	n.d.	AB104619 <b>BAC57896.1</b>	
endo-1,4-glucanase	<i>Prevotella ruminicola</i>	3.2.1.4	AB022867 BAA74515.1	<b>Q9ZN63</b>
endo-1,4-glucanase (ORF4)	<i>Prevotella ruminicola</i>	3.2.1.4	U96771 AAC97596.1	<b>O06842</b>
xylanase	<i>Prevotella ruminicola</i>	3.2.1.8	M83379 AAC36862.1	<b>Q45397</b>
cellulase (PhEG)	<i>Psacothoea hilaris</i>	n.d.	AB080266 <b>BAB86867.1</b>	
CelG	<i>Pseudoalteromonas haloplanktis A23</i>	3.2.1.4	Y17552 CAA76775.1	<b>O86099</b>
PP1682	<i>Pseudomonas putida KT2440</i>	n.d.	AE016780 <b>AAN67303.1</b> NC_002947 NP_743839.1	
$\beta$ -1,4-mannanase (AmnA)	<i>Pseudomonas sp. ND137</i>	n.d.	AB063258 <b>BAB79290.1</b> AB063258 <b>BAB79290.2</b>	
cellulase (AclA)	<i>Pseudomonas sp. ND137</i>	n.d.	AB063256 <b>BAB79288.1</b>	
PSPTO0905	<i>Pseudomonas syringae pv. tomato str. DC3000</i>	n.d.	AE016859 <b>AAO54439.1</b> NC_004578 NP_790744.1	
PSPTO3292	<i>Pseudomonas syringae pv. tomato str. DC3000</i>	n.d.	AE016867 <b>AAO56770.1</b> NC_004578 NP_793075.1	
ORF PAB0632	<i>Pyrococcus abyssi</i>	n.d.	AJ248285 <b>CAB49854.1</b> NC_000868 NP_126623.1	<b>Q9V052</b>
endoglucanase (PH1171)	<i>Pyrococcus horikoshii OT3</i>	3.2.1.4	AP000005 BAA30271.1 NC_000961 NP_143072.1	<b>O58925</b>
endo-1,4-glucanase	<i>Ralstonia solanacearum AW</i>	3.2.1.4	M84922 AAA61980.1	<b>P17974</b>
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2047</i>	n.d.	AF295262 <b>AAK97112.1</b>	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2957</i>	n.d.	AF295265 <b>AAK97115.1</b>	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2958</i>	n.d.	AF295266 <b>AAK97116.1</b>	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2972</i>	n.d.	AF295264 <b>AAK97114.1</b>	
endoglucanase	<i>Ralstonia solanacearum CFBP3059</i>	n.d.	AF295270 <b>AAK97120.1</b>	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP3858</i>	n.d.	AF295259 <b>AAK97109.1</b>	
ndoglucanase (fragment)	<i>Ralstonia solanacearum CFBP712</i>	n.d.	AF295267 <b>AAK97117.1</b>	
ndoglucanase (fragment)	<i>Ralstonia solanacearum CFBP715</i>	n.d.	AF295268 <b>AAK97118.1</b>	
endoglucanase	<i>Ralstonia solanacearum</i>	n.d.	AF295274 <b>AAK97124.1</b>	



	CFBP734				
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> GMI1000	n.d.	AF295251	AAK97101.1	
ORF Egl	<i>Ralstonia solanacearum</i> GMI1000	3.2.1.4	AL646076	CAD17313.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> ICMP7963	n.d.	AF295263	AAK97113.1	
endoglucanase	<i>Ralstonia solanacearum</i> J25	n.d.	AF295279	AAK97129.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> J25	n.d.	AF295276	AAK97126.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> JT516	n.d.	AF295258	AAK97108.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> JT523	n.d.	AF295252	AAK97102.1	
endoglucanase	<i>Ralstonia solanacearum</i> JT525	n.d.	AF295272	AAK97122.1	
endoglucanase	<i>Ralstonia solanacearum</i> JT528	n.d.	AF295273	AAK97123.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> MAFF211266	n.d.	AF295250	AAK97100.1	
endoglucanase	<i>Ralstonia solanacearum</i> NCPB1018	n.d.	AF295271	AAK97121.1	
endoglucanase	<i>Ralstonia solanacearum</i> NCPB283	n.d.	AF295275	AAK97125.1	
ndoglucanase (fragment)	<i>Ralstonia solanacearum</i> NCPB3190	n.d.	AF295253	AAK97103.1	
endoglucanase	<i>Ralstonia solanacearum</i> NCPB342	n.d.	AF295278	AAK97128.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> NCPB3987	n.d.	AF295261	AAK97111.1	
endoglucanase	<i>Ralstonia solanacearum</i> NCPB505	n.d.	AF295277	AAK97127.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> R230	n.d.	AF295280	AAK97130.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> R292	n.d.	AF295255	AAK97105.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW151	n.d.	AF295254	AAK97104.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW162	n.d.	AF295256	AAK97106.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW469	n.d.	AF295269	AAK97119.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW477	n.d.	AF295260	AAK97110.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW9	n.d.	AF295257	AAK97107.1	
endoglycoceramidase	<i>Rhodococcus</i> sp. C9	3.2.1.123	AB042327	BAB17317.1	
endoglycoceramidase II	<i>Rhodococcus</i> sp. M-777	3.2.1.123	U39554	AAB67050.1	O33853
endo-1,4-glucanase I	<i>Robillarda</i> sp. Y-20 ( <i>Pestalotiopsis</i> sp.)	3.2.1.4	AB030819	BAA90480.1	P23044
ndo-1,4-glucanase 4	<i>Ruminococcus albus</i>	3.2.1.4	AB016777	BAA32286.1	Q07940
endo-1,4-glucanase A	<i>Ruminococcus albus</i>	3.2.1.4	D16315	BAA32286.1	
			L10243	AAA26467.1	P23660
			X54931	CAA38692.1	Q59733
endo-1,4-glucanase B	<i>Ruminococcus albus</i>	3.2.1.4	X54932	CAA38693.1	P23661
endo-1,4-glucanase I	<i>Ruminococcus albus</i>	3.2.1.4	M30928	AAA26469.1	P16216
xylanase (fragment)	<i>Ruminococcus albus</i>	n.d.	AB057589	BAB39494.1	
			AB057589	BAB39495.1	
$\beta$ -1,4-endoglucanase VII	<i>Ruminococcus albus</i> F-	3.2.1.4	AB028321	BAA92430.1	

(EgVII)	40			
endo-1,4-glucanase V (EgV)	<i>Ruminococcus albus</i> F-40	3.2.1.4	AB028320 <b>BAA92146.1</b>	
endo-1,4-glucanase A (EndA)	<i>Ruminococcus flavefaciens</i> 17	3.2.1.4	S55178 AAB19708.1 Z83304 CAB05881.1	<b>O05143</b> <b>Q53302</b>
cellodextrinase	<i>Ruminococcus flavefaciens</i> FD-1	3.2.1.-	X51944 CAA36207.1	<b>P16169</b>
EXG1	<i>Saccharomyces bayanus</i> 623-6C	n.d.	AY144818 <b>AAO32382.1</b>	
SPR1	<i>Saccharomyces bayanus</i> 623-6C	n.d.	AY144819 <b>AAO32383.1</b>	
EXG1 (fragment)	<i>Saccharomyces castellii</i> CBS4309	n.d.	AY144925 <b>AAO32489.1</b>	
EXG1 (fragment)	<i>Saccharomyces castellii</i> CBS4309	n.d.	AY144926 <b>AAO32490.1</b>	
exo-1,3-glucanase (sporulation)	<i>Saccharomyces cerevisiae</i> GRF88	3.2.1.58	S52935 AAB24895.1 X59259 CAA41952.1 Z75098 CAA99399.1	<b>P32603</b>
exo-1,3-glucanase 1	<i>Saccharomyces cerevisiae</i> S288C	3.2.1.58	M34341 AAA34599.1 U17243 AAB67345.1 NC_001144 NP_013403.1	<b>P23776</b>
exo-1,3-glucanase 2	<i>Saccharomyces cerevisiae</i> S288C	3.2.1.58	Z46870 CAA86950.1 Z68329 CAA92719.1 Z70202 CAA94100.1 NC_001136 NP_010547.1	<b>P52911</b>
ORF YBR056W	<i>Saccharomyces cerevisiae</i> S288C	n.d.	Z35925 CAA84999.1 Z46260 CAA86399.1 NC_001134 NP_009612.1	<b>P38081</b>
ORF YIB7W	<i>Saccharomyces cerevisiae</i> S288C	n.d.	Z37996 CAA86077.1 Z38062 CAA86209.1 NC_001141 NP_012272.1	<b>P40566</b>
EXG1	<i>Saccharomyces kluyveri</i> CBS3082	n.d.	AY145000 <b>AAO32563.1</b>	
endo-1,4-glucanase I (fragment)	<i>Schizophyllum commune</i>	3.2.1.4		<b>P81190</b>
exo-1,3-glucanase (SPAC12B10.11)	<i>Schizosaccharomyces pombe</i> 972h-	3.2.1.58	Z70721 CAA94701.1 NC_003424 NP_594643.1	<b>Q10444</b>
ORF SPBC1105.05	<i>Schizosaccharomyces pombe</i> 972h-	n.d.	AL096851 <b>CAB50968.1</b> NC_003423 NP_596461.1	
ORF SPBC2D10.05	<i>Schizosaccharomyces pombe</i> 972h-	n.d.	NC_003423.1 <b>NP_596224.1</b>	
endoglucanase S (EndS)	<i>Sinorhizobium meliloti</i>	3.2.1.4	AF233448 <b>AAG44364.1</b>	
cellulase	<i>Stigmatella aurantiaca</i> Sg a15	n.d.	AJ421825 <b>CAD19084.1</b>	
ORF ManA2 (SC2H4.16)	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL031514 CAA20610.1 NC_003888 NP_630335.1	<b>O86599</b>
ORF SC10F4.10c	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL450350 <b>CAC16970.1</b> NC_003888 NP_631677.1	<b>Q9F3Q0</b>
ORF SC6D11.02c	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL158061 <b>CAB76325.1</b> NC_003888 NP_631455.1	
ORF SCF11.34c (ManA)	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL121746 CAB57406.1 AL132662 CAB59611.1 AL939106 <b>CAD55266.1</b>	
ORF SCF51A.35	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL121596 <b>CAB56687.1</b> NC_003888 NP_624777.1	
ORF SCM11.04c	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL133278 CAB61915.1 NC_003888 NP_625246.1	
chitosanase II (Choll)	<i>Streptomyces griseus</i> HUT 6037	3.2.1.132	AB088201 <b>BAC65342.1</b>	
endo-1,4-glucanase	<i>Streptomyces lividans</i>	3.2.1.4	M82807 -	<b>P27035</b>
$\beta$ -mannanase	<i>Streptomyces lividans</i>	3.2.1.78	M92297 AAA26710.1	<b>P51529</b>

ORF SSO3007	66	<i>Sulfolobus solfataricus</i>	n.d.	AE006891 AAK43109.1 AL512980 <b>CAC24030.1</b> NC_002754 NP_344319.1		
endo- $\beta$ -1,4 glucanase (Eg1)		<i>Talaromyces emersonii</i>	3.2.1.4	AF440003 AAL33630.1 AF440013 <b>AAL33639.1</b>		
ORF TTE0061		<i>Thermoanaerobacter tengcongensis MB4T</i>	n.d.	AE012980 <b>AAM23368.1</b>	Q8RDH1	
ORF TTE0359		<i>Thermoanaerobacter tengcongensis MB4T</i>	n.d.	AE013009 <b>AAM23649.1</b>	Q8RCQ7	
$\beta$ -mannanase A		<i>Thermoanaerobacterium polysaccharolyticum KM-THCJ</i>	3.2.1.78	U82255 <b>AAD09354.1</b>	Q9ZA17	
$\beta$ -1,4-glucanase (ENG1)		<i>Thermoascus aurantiacus IFO 9748</i>	3.2.1.4	AY055121 AAL16412.1 AF487830 <b>AAL88714.2</b>		1GZJ A 1H1N A
endo-1,4-glucanase E5	Cel5A	<i>Thermobifida fusca</i>	3.2.1.4	L01577 AAC09379.1	<b>Q01786</b>	
$\beta$ -mannanase (Man)		<i>Thermobifida fusca</i> ( <i>Thermomonospora fusca</i> )	3.2.1.78	AJ006227 CAA06924.1		<b>1BQC A</b> 2MAN A 3MAN A
endo-1,4-glucanase		<i>Thermophilic anaerobe NA10</i>	3.2.1.4	AB008029 BAA22939.1	<b>O24820</b>	
ORF TVG0696003		<i>Thermoplasma volcanium GSS1</i>	n.d.	AP000993 <b>BAB59829.1</b> NC_002689 NP_111209.1	Q97AX2	
$\beta$ -mannanase (ManB;TM1227)	Man5	<i>Thermotoga maritima</i>	3.2.1.78	AE001779 AAD36302.1 Y17980 CAB56854.1 NC_000853 NP_229032.1	<b>Q9X0V4</b>	
endoglucanase (TM1751)	Cel5A	<i>Thermotoga maritima</i>	3.2.1.4	AE001813 AAD36816.1 NC_000853 NP_229549.1	<b>Q9X273</b>	
ORF TM1752	Cel5B	<i>Thermotoga maritima</i>	n.d.	AE001813 AAD36817.1 NC_000853 NP_229550.1	<b>Q9X274</b>	
$\beta$ -mannosidase		<i>Thermotoga neapolitana</i>	3.2.1.25	AY033477 AAK53459.1 Y17981 <b>CAB56856.1</b>		
cellulase		<i>Thermus caldophilus</i>	3.2.1.4	AF289822 <b>AAK60011.1</b>		
endo-1,6-glucanase		<i>Trichoderma harzianum</i>	3.2.1.75	X79197 CAA55789.1	Q12711 <b>Q12712</b>	
$\beta$ -mannanase		<i>Trichoderma reesei</i> ( <i>Hypocrea jecorina</i> )	3.2.1.78	L25310 AAA34208.1	<b>Q99036</b>	1QNO A 1QNP A 1QNQ A 1QNR A 1QNS A
endo-1,4-glucanase II	Cel5A	<i>Trichoderma reesei</i> ( <i>Hypocrea jecorina</i> )	3.2.1.4	M19373 AAA34213.1	<b>P07982</b>	
endo-1,4-glucanase II		<i>Trichoderma viride</i>	3.2.1.4	AB021657 BAA36216.1	<b>O93833</b>	
endo-1,4-glucanase (Cel)		<i>Unidentified bacterium</i>	3.2.1.4	U12011 AAA91966.1	<b>Q60054</b>	
Sequence 1 from patent US 6190899		<i>Unknown</i>	n.d.	<b>AAE60112.1</b>		
Sequence 2 from patent US 6440911		<i>Unknown.</i>	n.d.	<b>AAN27517.1</b>		
Sequence 4 from patent US 6440911		<i>Unknown.</i>	n.d.	<b>AAN27518.1</b>		
$\beta$ -mannanase		<i>Vibrio sp. MA-138</i>	3.2.1.78	D86329 BAA25188.1	<b>O69347</b>	
endoglucanase		<i>Volvariella volvacea V14</i>	3.2.1.4	AF329732 <b>AAG59832.1</b>		
endo-1,4-glucanase (ENG)		<i>Xanthomonas albilineans</i>	3.2.1.4	L26543 AAA27599.1	<b>Q60100</b>	
ORF Egl		<i>Xanthomonas axonopodis pv. citri str. 306</i>	n.d.	AE011625 AAM34920.1 NC_003919 <b>NP_640384.1</b>		
ORF Egl		<i>Xanthomonas axonopodis pv. citri str. 306</i>	n.d.	AE011626 AAM34921.1 NC_003919 <b>NP_640385.1</b>		

ORF Egl	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011626 <b>AAM34922.1</b> NC_003919 <b>NP_640386.1</b>	
ORF EngXCA	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011689 <b>AAM35501.1</b> NC_003919 <b>NP_640965.1</b>	
ORF XAC0346	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011660 <b>AAM35238.1</b> NC_003919 <b>NP_640702.1</b>	
ORF XAC0933 (fragment)	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011724 <b>AAM35821.1</b> NC_003919 <b>NP_641285.1</b>	
ORF XAC0934 (fragment)	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011724 <b>AAM35822.1</b> NC_003919 <b>NP_641286.1</b>	
ORF XAC1796	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011812 <b>AAM36659.1</b> NC_003919 <b>NP_642123.1</b>	
endo-1,4-glucanase	<i>Xanthomonas campestris</i>	3.2.1.4	M32700 <b>AAA27612.1</b> AJ304415 <b>CAC18529.1</b>	P19487
EngXCA	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012472 <b>AAM42791.1</b> NC_003902 <b>NP_638867.1</b>	
ORF Egl	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012095 <b>AAM39345.1</b> NC_003902 <b>NP_635421.1</b>	
ORF Egl	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012096 <b>AAM39346.1</b> NC_003902 <b>NP_635422.1</b>	
ORF Egl	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012096 <b>AAM39347.1</b> NC_003902 <b>NP_635423.1</b>	
ORF XCC0857	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012185 <b>AAM40172.1</b> NC_003902 <b>NP_636248.1</b>	
ORF XCC1778	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012279 <b>AAM41068.1</b> NC_003902 <b>NP_637144.1</b>	
ORF XCC3535	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012474 <b>AAM42805.1</b> NC_003902 <b>NP_638881.1</b>	
ORF XF0810	<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003920 <b>AAF83620.1</b> NC_002488 <b>NP_298100.1</b>	Q9PF68
ORF XF0818	<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003921 <b>AAF83628.1</b> NC_002488 <b>NP_298108.1</b>	Q9PF60
ORF XF2708	<i>Xylella fastidiosa</i> 9a5c	n.d.	AE004077 <b>AAF85505.1</b> NC_002488 <b>NP_299985.1</b>	Q9PA12
Egl	<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012561 <b>AAO29885.1</b> NC_004556 <b>NP_780236.1</b>	
EngXCA	<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012560 <b>AAO29683.1</b> NC_004556 <b>NP_780034.1</b>	
EngXCA	<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012560 <b>AAO29688.1</b> NC_004556 <b>NP_780039.1</b>	
exo-1,3-glucanase	<i>Yarrowia lipolytica</i>	3.2.1.58	Z46872 <b>CAA86952.1</b>	Q12725

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# CAZy - Carbohydrate-Active enZYmes

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## Introduction to Carbohydrate- Binding Module Families

Carbohydrate-  
Binding  
Modules

Last updated on  
2003 Apr 1

### Introduction

A **carbohydrate-binding module (CBM)** is defined as contiguous amino acid sequence within a carbohydrate-active enzyme with a discreet fold having **carbohydrate-binding activity**. A few exceptions are CBMs in cellulosomal scaffoldin proteins and rare instances of independent putative CBMs. The requirement of CBMs existing as modules within larger enzymes sets this class of carbohydrate-binding protein apart from other non-catalytic sugar binding proteins such as lectins and sugar transport proteins.

CBMs were previously classified as cellulose-binding domains (CBDs) based on the initial discovery of several modules that bound cellulose [1, 2]. However, additional modules in carbohydrate-active enzymes are continually being found that bind carbohydrates other than cellulose yet otherwise meet the CBM criteria, hence the need to reclassify these polypeptides using more inclusive terminology.

### Family classification

Previous classification of cellulose-binding domains were based on amino acid similarity [3]. Groupings of CBDs were called "Types" and numbered with roman numerals (e.g. Type I or Type II CBDs). In keeping with the glycoside hydrolase classification, these groupings are now called families and numbered with Arabic numerals. Families 1 to 13 are the same as Types I to XIII [3].

The family classification of CBMs is expected to:

1. aid in the identification of CBMs
2. in some cases, predict binding specificity
3. aid in identifying functional residues
4. reveal evolutionary relationships
5. be predictive of polypeptide folds

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This document provides an updated list of the CBM-containing proteins, arranged by CBM family. When a protein contains CBDs from **different** families, it appears in **each** appropriate family. Because the fold of proteins is better conserved than their sequences, some of the CBM families are likely to form **superfamilies** or **clans**.

## References

1. Tomme, P. & Claeyssens, M. (1989) Identification of the functional important carboxylgroup in cellobiohydrolase I from *Trichoderma reesei* : a chemical modification study. FEBS Lett. 243, 239-243
2. Gilkes, N.R., Warren, R.A., Miller, R.C.J. & Kilburn, D.G. (1988) Precise excision of the cellulose binding domains from two *Cellulomonas fimi* cellulases by a homologous protease and the effect on catalysis. J.Biol.Chem. 263, 10401-10407
3. Tomme, P., Warren, R.A., Miller, R.C., Jr., Kilburn, D.G. & Gilkes, N.R. (1995) in Enzymatic Degradation of Insoluble Polysaccharides (Saddler, J.N. & Penner, M., eds.), Cellulose-binding domains: classification and properties. pp. 142-163, American Chemical Society, Washington

## Note

The GenBank, SWISS-PROT, and/or PDB entries for these proteins are therefore mentioned in each of the relevant list of family members.

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## Family CBM3

Family CBM3

**CAZy Family** Carbohydrate-Binding Module Family 3

**Description** Carbohydrate-binding module 3. Modules of approx. 150 residues found in bacterial enzymes. The cellulose-binding function has been demonstrated in many cases. In one instance binding to chitin has been reported.

**3D Structure Status** Available (see PDB). Fold  $\beta$ -sandwich

**Note** Previously known as cellulose-binding domain family III (CBD III).

**Relevant Links** HOMSTRAD; InterPro; PFAM

**Statistics** CAZy(62); GenBank/GenPept (71); Swissprot (45); PDB (10); 3D(4)

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
scaffoldin CipV	<i>Acetivibrio cellulolyticus</i>	n.d.	AF155197 <b>AAF06064.1</b>	Q9RPL0	
cellulase CelA	<i>Anaerocellum thermophilum</i>	3.2.1.91 3.2.1.4	Z86105 CAB06786.1	<b>P96311</b>	
endoglucanase A (EngA)	<i>Bacillus amyloliquefaciens</i> <i>UMAS1002</i>	n.d.	AF363635 <b>AAL99668.1</b>		
endo-1,4-glucanase 3a	<i>Bacillus lautus</i>	3.2.1.4	A28175 <b>CAA01935.1</b>		
ORF 1	<i>Bacillus lautus</i>	n.d.	M76588 <b>AAA22302.1</b>	<b>P29718</b>	
endoglucanase	<i>Bacillus pumilus</i> S-27	3.2.1.4	AF206716 <b>AAF15367.1</b>		
endo-1,4-glucanase	<i>Bacillus</i> sp. 5H	3.2.1.4	AB016164 BAA31712.1	<b>O83012</b>	
CelS	<i>Bacillus</i> sp. 79-23	3.2.1.4	AF045482 AAC02536.1	<b>O52731</b>	
endoglucanase CelB	<i>Bacillus</i> sp. BP23	3.2.1.4	AJ133614 CAB38941.1	<b>Q9Z411</b>	
endo-1,4-glucanase	<i>Bacillus</i> sp. D04	3.2.1.4	U27084 AAC43478.1	<b>Q45430</b>	
endo-1,4-glucanase IV	<i>Bacillus</i> sp. KSM-522	3.2.1.4	AB004098 BAA24918.1	<b>O50589</b> P28622	
endo-1,4-glucanase	<i>Bacillus subtilis</i>	3.2.1.4	M28332 AAA22307.1	<b>Q45532</b>	
endo-1,4-glucanase	<i>Bacillus subtilis</i> BSE616	3.2.1.4	D01057 BAA00859.1	<b>P23549</b>	
endo-1,4- $\beta$ -glucanase	<i>Bacillus subtilis</i> CHZ1	3.2.1.4	AY044252 <b>AAK94871.1</b>		
endo-1,4-glucanase	<i>Bacillus subtilis</i> DLG	3.2.1.4	M16185 AAA22496.1	<b>P07983</b>	
endo-1,4-glucanase (EglS or BglC)	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	3.2.1.4	AF355629 AAK39540.1 X04689 CAA28392.1 X67044 CAA47429.1 Z29076 CAA82317.1 Z73234 CAA97610.1 Z99113 CAB13696.1 NC_000964 NP_389695.1	<b>P10475</b>	
scaffoldin CipBc	<i>Bacteroides cellulosolvens</i>	none	AF224509 <b>AAG01230.1</b>	Q9FDJ9	
$\beta$ -1,4-mannanase (ManA)	<i>Caldibacillus cellulovorans</i>	3.2.1.78	AF163837 <b>AAF22274.1</b>	Q9RFX5	



ORF (fragment)		<i>Caldibacillus cellulovorans</i>	n.d.	AF200304 <b>AAF61648.1</b>	
ORF1 (fragment)		<i>Caldibacillus cellulovorans</i>	n.d.	AF163837 <b>AAF22273.1</b>	
xylanase XynA		<i>Caldibacillus cellulovorans</i>	3.2.1.8	AF200304 <b>AAF61649.1</b>	
$\beta$ -mannanase/endo-1,4-glucanase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.4 3.2.1.78	L01257 AAA71887.1	<b>P22533</b>
CelA		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.4	L32742 AAA91086.1	<b>P22534</b>
endo-1,4-glucanase/cellobiohydrolase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.91 3.2.1.4	X13602 CAA31936.1	<b>P10474</b>
xynC (multidomain protein)		<i>Caldicellulosiruptor sp. Rt69B.1</i>	3.2.1.8	AF036924 AAB95326.1	<b>O52374</b>
CelB (multidomain protein)		<i>Caldicellulosiruptor sp. Tok7B.1</i>	n.d.	AF078737 <b>AAD30364.1</b>	Q9X3P6
ORF5		<i>Caldicellulosiruptor sp. Tok7B.1</i>	n.d.	AF078038 <b>AAK06388.1</b>	
xylanase/arabinosidase XynA		<i>Caldicellulosiruptor sp. Tok7B.1</i>	3.2.1.8 3.2.1.55	AF078737 <b>AAD30363.1</b>	Q9X3P5
endo-1,4-glucanase B	<i>Cel9A</i>	<i>Cellulomonas fimi</i>	3.2.1.4	M64644 AAA23086.1	<b>P26225</b>
ORF CAC0910		<i>Clostridium acetobutylicum ATCC 824</i>	n.d.	AE007606 <b>AAK78886.1</b>	Q977Y4
ORF CAC0913		<i>Clostridium acetobutylicum ATCC 824</i>	n.d.	AE007607 AAK78889.1	<b>Q97KK5</b>
ORF CAC0916		<i>Clostridium acetobutylicum ATCC 824</i>	n.d.	AE007607 AAK78892.1	<b>Q97KK3</b>
cellulase H (CelH)	<i>Cel9H</i>	<i>Clostridium cellulolyticum</i>	3.2.1.4	AF316823 AAG45157.1	<b>Q9EYQ5</b>
cellulase J (CelJ)	<i>Cel9J</i>	<i>Clostridium cellulolyticum</i>	3.2.1.4	AF316823 AAG45158.1	<b>Q9EYQ4</b>
endo-1,4-glucanase G (CelCG)	<i>Cel9G</i>	<i>Clostridium cellulolyticum</i>	3.2.1.4	M87018 AAA73868.1	<b>P37700</b> 1G87 1GA2 1K72 1KFG 1G43 A
scaffoldin CipC		<i>Clostridium cellulolyticum</i>	none	U40345 AAC28899.1	<b>Q45996</b>
endo-1,4-glucanase H (fragment)		<i>Clostridium cellulovorans</i>	3.2.1.4	U34793 AAC38572.2	<b>O65987</b>
scaffoldin CbpA		<i>Clostridium cellulovorans</i>	none	M73817 AAA23218.1	<b>P38058</b>
scaffoldin CipA		<i>Clostridium josui</i>	none	AB004845 <b>BAA32429.1</b>	
cellobiohydrolase Y (avicelase II) (CelY)		<i>Clostridium stercoararium</i>	3.2.1.91	Z69359 CAA93280.1	<b>P50900</b>
endo-1,4-glucanase Z (avicelase I) (CelZ)		<i>Clostridium stercoararium</i>	3.2.1.4	X55299 CAA39010.1	<b>P23659</b>
endoglucanase Q (CelQ)	<i>Cel9I</i>	<i>Clostridium thermocellum</i>	3.2.1.4	AB047845 <b>BAB33148.1</b>	
scaffoldin CipA		<i>Clostridium thermocellum ATCC 27405</i>	none		<b>Q06851</b> 1NBC A
ORFZ		<i>Clostridium thermocellum DSM 1237</i>	n.d.	Z68924 CAA93151.2 AJ420770 CAD12660.1	<b>Q46392</b>
1,4- $\beta$ -cellobiohydrolase (CelO)		<i>Clostridium thermocellum F7</i>	3.2.1.91	AJ275975 <b>CAB76938.1</b>	
cellobiohydrolase A (CbhA)		<i>Clostridium thermocellum F7</i>	3.2.1.91	X80993 CAA56918.1	<b>Q59325</b>
endo-1,4-glucanase (CelN)		<i>Clostridium thermocellum F7</i>	3.2.1.4	AJ275974 <b>CAB76935.1</b>	

endo-1,4-glucanase F	Cel9B	<i>Clostridium thermocellum</i>	3.2.1.4	X60545 CAA43035.1	<b>P26224</b>	
		NCIB 10682				
endo-1,4-glucanase I (Cell or CMC)	Cel9C	<i>Clostridium thermocellum</i>	3.2.1.4	L04735 AAA20892.1	<b>Q02934</b>	
		NCIB10682 / F7		AJ275974 CAB76932.1		
endo-1,4-glucanase N		<i>Erwinia carotovora</i>	3.2.1.4	L39788 AAC37033.1	<b>Q59394</b>	
		atroseptica				
endo-1,4-glucanase V1		<i>Erwinia carotovora</i>	3.2.1.4	X79241 CAA55823.1	<b>Q59395</b>	
		SCC3193				
endo-1,4-glucanase V		<i>Erwinia carotovora</i>	3.2.1.4	X76000 CAA53592.1	<b>Q47096</b>	
		SCRI193				
endo-1,4-glucanase CelA (fragment)		<i>Erwinia carotovora</i>	3.2.1.4	AF025768 AAC02964.1	<b>O31029</b>	
		subsp. carotovora LY34				
cellulose-binding protein E1 (Cbpe1)		<i>Eubacterium</i>	n.d.	AB072270 BAB86305.1		
		cellulosolvens				
endo-1,4-glucanase A		<i>Paenibacillus lautus</i>	3.2.1.4	M76588 AAA22303.1	<b>P29719</b>	
cellobiohydrolase Cel48C	Cel48C	<i>Paenibacillus</i> sp. BP-23	3.2.1.91	AJ488933 CAD32945.1		
cellulase VI (Cel9A)	Cel9A	<i>Ruminococcus albus</i> F-40	n.d.	AB028321 BAB64431.1		
ORF SCF11.15		<i>Streptomyces coelicolor</i>	n.d.	AL132662 CAB59592.1		
		A3(2)		NC_003888 NP_624849.1		
endo/exo-1,4-glucanase E4	Cel9A	<i>Thermobifida fusca</i>	3.2.1.4	L20093 AAB42155.1	<b>P26221</b>	1JS4 A
			3.2.1.91		<b>Q08167</b>	1TF4 A
						3TF4 A
						4TF4 A
endo-1,4-glucanase		<i>Thermophilic anaerobe</i>	3.2.1.4	AB008029 BAA22939.1	<b>O24820</b>	
		NA10				
Sequence from patent		Unknown	none	- AAE16382.1		
				- AAO30719.1		
Sequence 10 from patent US 6429000		Unknown.	n.d.	AAN26180.1		

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# CAZy - Carbohydrate-Active enZymes

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Family **CBM2**

Family CBM2

**CAZy Family** Carbohydrate-Binding Module Family 2

**Description** Carbohydrate-binding module 2. Modules of approx. 100 residues and which are found in a large number of bacterial enzymes. The cellulose-binding function has been demonstrated in many cases. Several of these modules have been shown to also bind chitin or xylan.

**3D Structure Status** Available (see PDB)

**Note** Previously known as cellulose-binding domain family II (CBD II).

**Relevant Links** HOMSTRAD; InterPro; PFAM

**Statistics** CAZy(107); GenBank/GenPept (143); Swissprot (83); PDB (10); 3D(11)

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
endo-1,4-glucanase	<i>Acidothermus cellulolyticus</i>	3.2.1.4	U33212 AAA75477.1 AX467594 CAD42489.1	<b>P54583</b>	3D
endo-1,4-glucanase	<i>Actinomyces</i> sp. 40	3.2.1.4	U94825 AAC06196.1	<b>O66064</b>	
ORF PCZA361.11 (putative oxidoreductase)	<i>Amycolatopsis orientalis</i>	n.d.	AJ223998 CAA11769.1	<b>O52799</b>	
ORF egl	<i>Azorhizobium caulinodans</i> ORS571	n.d.	Z48958 -		
BA_0961	<i>Bacillus anthracis</i> str. A2012	n.d.	NC_003995 NP_654321.1		
chitinase CW (ChiCW)	<i>Bacillus cereus</i> 28-9	3.2.1.14	AF416570 AAM48520.1		
chitinase B	<i>Bacillus cereus</i> CH	3.2.1.14	AB041932 BAB16891.1	Q9FAC8	
chitinase	<i>Bacillus thuringiensis</i>	3.2.1.14	U89796 AAB58579.1	<b>O07088</b>	
chitinase (Chi)	<i>Bacillus thuringiensis</i>	3.2.1.14	AF424979 AAL17867.1 AY074882 AAL71886.2		
chitinase	<i>Bacillus thuringiensis</i> serovar israelensis	n.d.	AF526379 AAM88400.1		
chitinase (Kchi)	<i>Bacillus thuringiensis</i> serovar kurstaki	n.d.	AY189740 AAO34713.1		
chitinase	<i>Bacillus thuringiensis</i> serovar sotto	n.d.	AY129671 AAM94024.1		
endo-1,4-glucanase 1	<i>Butyrivibrio fibrisolvens</i> H17c	3.2.1.4	- AAE29745 X17538 CAA35574.1	<b>P20847</b>	
cellobiohydrolase A	Cel6B <i>Cellulomonas fimi</i>	3.2.1.91	L25809 AAC36898.1	<b>P50401</b>	
cellobiohydrolase B	Cel48A <i>Cellulomonas fimi</i>	3.2.1.91	L38827 AAB00822.1	<b>P50899</b>	
endo-1,4-glucanase A	Cel6A <i>Cellulomonas fimi</i>	3.2.1.4	M15823 AAA23084.1	<b>P07984</b>	
endo-1,4-glucanase B	Cel9A <i>Cellulomonas fimi</i>	3.2.1.4	M64644 AAA23086.1	<b>P26225</b>	
endo-1,4-glucanase D	Cel5A <i>Cellulomonas fimi</i>	3.2.1.4	L02544 AAA23089.1	<b>P50400</b>	
xylanase (Cex)	Xyn10A <i>Cellulomonas fimi</i>	3.2.1.8	M15824 AAA56791.1 L11080 AAA56792.1	P07986 <b>Q59277</b>	1EXG 1EXH
xylanase D	Xyn11A <i>Cellulomonas fimi</i>	3.2.1.8	X76729 CAA54145.1	<b>P54865</b>	1E5B A

			3.1.1.72			1E5C A 1HEH C 1HEJ C 1XBD _ 2XBD _
endo-1,4-glucanase B (cflB)	<i>Cellulomonas flavigena</i>		3.2.1.4	AF172345 <b>AAD48494.2</b>		
xylanase (fragment)	<i>Cellulomonas flavigena</i> CDBB5321		3.2.1.8	AF338352 <b>AAK15536.1</b>	Q9AG99	
xylanase	<i>Xyn11A Cellulomonas pachnodae</i>		3.2.1.8	AF120156 <b>AAD54767.1</b>	Q9RQB8	
chitinase 63 (Chi63)	<i>Cellulomonas sp. GM13</i>		3.2.1.14	AF181718 <b>AAF00931.2</b>		
endo-b1,4-mannanase 5B	<i>Man5B Cellvibrio japonicus</i>		n.d.	AY187032 <b>AAO31760.1</b>		
arabinofuranosidase C	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.55	X54523 CAA38390.1	<b>P23031</b>	
cellodextrinase C	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.-	X61299 CAA43597.1	<b>P27033</b>	
endo-1,4-glucanase A	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.4	X12570 CAA31082.1	<b>P10476</b>	
endo-1,4-glucanase B	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.4	X52615 CAA36844.1	<b>P18126</b>	
endo-1,4-glucanase E	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.4	X86798 CAA60493.1	<b>Q59665</b>	
esterase D	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		n.d.	X58956 CAA41727.1	<b>Q51815</b>	
pectate lyase (PelA)	<i>Pel10A Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		4.2.2.2	AF279264 <b>AAG29353.1</b>	Q9F7L3	3D
rhamnogalacturonan lyase	<i>Rgl11A Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		4.2.2.-	AY026755 <b>AAK20911.1</b>	Q9AF09	
xylanase A	<i>Xyn10A Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.8	X15429 CAA33469.1	<b>P14768</b>	3D
xylanase B	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i> )		3.2.1.8	X54523 CAA38389.1	<b>P23030</b>	
chitinase vChti-1	<i>Chlorella virus CVK2</i>		3.2.1.14	AB022343 <b>BAA78554.1</b>	Q9WAX4	
Cellulase CelA	<i>Clavibacter michiganensis</i> NCPB 382		3.2.1.4	X62582 <b>CAA44467.2</b>	Q9K5C7	
cellulase CelA	<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>		3.2.1.4	AY007311 <b>AAK16222.1</b>	Q9AF65	
endo-1,4-glucanase D	<i>Clostridium cellulovorans</i>		3.2.1.4	M37434 AAA23233.1	<b>P28623</b>	
endo-1,4-glucanase (CelA)	<i>Clostridium longisporum</i>		3.2.1.4	L02868 AAC37035.1	<b>P54937</b>	
CMC-xylanase (fragment)	<i>Fibrobacter succinogenes</i> S85		3.2.1.4 3.2.1.8	U94826 AAC06197.1	<b>O66065</b>	
endoglucanase 1 (Eng1)	<i>Globodera rostochiensis</i>		3.2.1.4	AF004523 AAC48325.1 AF056110 AAC63988.1	<b>O16028</b>	
endoglucanase 1 (Eng1)	<i>Heterodera glycines</i>		3.2.1.4	AF052733 AAC15707.1 AF006052 AAC48327.1 A79341 CAB59144.1	<b>O18453</b>	
$\beta$ -1,4-endoglucanase Eng-1a	<i>Meloidogyne incognita</i>		3.2.1.4	AF323087 <b>AAK21882.1</b>	Q9BJZ1	
cellulose -binding protein	<i>Meloidogyne incognita</i>		none	AF049139 AAC05133.1	<b>O61530</b>	

endo-1,4-glucanase 1 (Eng-1)	<i>Meloidogyne incognita</i>	3.2.1.4	AF100549 <b>AAD45868.1</b>	Q9UA57
ORF X (fragment)	<i>Methylococcus capsulatus</i> <i>Bath</i>	n.d.	AF447860 <b>AAL40976.1</b>	
endo-1,4-glucanase A	<i>Microbispora bispora</i>	3.2.1.4		<b>P26414</b>
endo-1,4-glucanase	<i>Micromonospora</i> <i>cellulolyticum</i>	3.2.1.4	S76408 AAC60491.1	<b>Q53488</b>
ORF MT2041	<i>Mycobacterium tuberculosis</i> <i>CDC1551</i>	n.d.	AE007056 <b>AAK46316.1</b> NC_002755 NP_336502.1	
ORF Rv1987	<i>Mycobacterium tuberculosis</i> <i>H37Rv</i>	n.d.	Z74025 CAA98397.1 NC_000962 NP_216503.1	<b>Q10870</b>
endoxylanase (XynA)	<i>Nonomuraea flexuosa</i>	3.2.1.8	AJ508952 <b>CAD48747.1</b>	
ORF A181/182R	<i>Paramecium bursaria</i> <i>Chlorella virus 1</i>	3.2.1.14	U42580 AAC96549.2 NC_000852 NP_048529.1	<b>Q84501</b> <b>Q84502</b>
ORF PF1233	<i>Pyrococcus furiosus</i> DSM 3638	n.d.	AE010230 <b>AAL81357.1</b> NC_003413 NP_578962.1	Q8U1H5
ORF RSp0583	<i>Ralstonia solanacearum</i> <i>GMI1000</i>	n.d.	AL646079 <b>CAD17734.1</b> NC_003296 NP_522144.1	Q8XS97
chitinase C (2SC6G5.20c)	<i>Streptomyces coelicolor</i> A3 (2)	3.2.1.14	AB017010 BAA75644.1 AL359152 CAB94547.1 NC_003888 NP_629515.1	<b>Q9Z9M8</b>
ORF 2SCC13.07c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL442165 <b>CAC10108.1</b> NC_003888 NP_627029.1	Q9F3I2
ORF AxeA	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133220 <b>CAB61737.1</b> NC_003888 NP_626539.1	Q9RKN7
ORF CelB (SCG11A.18)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133210 <b>CAB61599.1</b> NC_003888 NP_625477.1	Q9RJY3
ORF CelS2 (SCG11A.19)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133210 <b>CAB61600.1</b> NC_003888 NP_625478.1	Q9RJY2
ORF SC10F4.10c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL450350 <b>CAC16970.1</b> NC_003888 NP_631677.1	Q9F3Q0
ORF SC4H2.07c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL022268 <b>CAA18323.1</b> NC_003888 NP_629910.1	O69962
ORF SC5C7.30c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL031515 CAA20642.1 NC_003888 NP_630626.1	<b>O86727</b>
ORF SC5C7.31c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL031515 CAA20643.1 NC_003888 NP_630627.1	<b>O86728</b>
ORF SC5C7.33	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL031515 CAA20645.1 NC_003888 NP_630629.1	<b>O86730</b>
ORF SC7H1.24	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL021411 CAA16211.1 NC_003888 NP_630071.1	<b>O54183</b>
ORF SCF11.34c (ManA)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL132662 CAB59611.1 AL939106 <b>CAD55266.1</b>	
ORF SCF91.34c (XlnA)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL132973 <b>CAB61191.1</b> NC_003888 NP_624983.1	Q9RJ91
ORF XlnB	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133220 <b>CAB61738.1</b> NC_003888 NP_626540.1	Q9RKN6
chitinase III (Chi III) (fragment)	<i>Streptomyces griseus</i> HUT 6037	3.2.1.14	AB081807 <b>BAB86377.1</b>	
cellulose binding protein (ORF2)	<i>Streptomyces halstedii</i>	n.d.	U51222 <b>AAC45430.1</b>	O07862
endo-1,4-glucanase	<i>Streptomyces halstedii</i>	3.2.1.4	U51222 AAC45429.1	<b>O08468</b>
xylanase	<i>Streptomyces halstedii</i> JM8	3.2.1.8	U41627 AAC45554.1	<b>Q59922</b> 1NQ6
acetyl xylan esterase	<i>Streptomyces lividans</i>	3.1.1.72	M64552 AAC06115.2	<b>Q54413</b>
chitinase C	<i>Streptomyces lividans</i>	3.2.1.14	D12647 BAA02168.1	<b>P36909</b>
endo-1,4-glucanase	<i>Streptomyces lividans</i>	3.2.1.4	M82807 -	<b>P27035</b>
endo-1,4-glucanase	<i>Streptomyces lividans</i>	3.2.1.4	U04629 AAB71950.1	<b>Q54331</b> 3D
xylanase B	<i>Streptomyces lividans</i>	3.2.1.8	M64552 AAC06114.2	<b>P26515</b>
chitinase C	<i>Streptomyces peucetius</i>	3.2.1.14	AF206633 <b>AAF43629.1</b>	Q9L8G0
chitinase-63	<i>Streptomyces plicatus</i>	3.2.1.14	M18397 AAA26717.1	<b>P11220</b>

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endo-1,4-glucanase S		<i>Streptomyces rochei</i> A2	3.2.1.4	M82804 AAA26720.1	
cellulase 12A	<i>Cel12A</i>	<i>Streptomyces</i> sp. 11AG8	3.2.1.4	X73953 CAA52139.1	<b>Q59963</b>
				AF233376 AAE59731.1	Q9KIH1 10A4
				<b>AAF91283.1</b>	
xylanase B		<i>Streptomyces thermocyaneoviolaceus</i>	3.2.1.8	AF194025 <b>AAF04601.1</b>	Q9RMM4
acetyl xylan esterase STX-III		<i>Streptomyces thermoviolaceus</i>	3.1.1.6	D85898 BAA19779.1	<b>O08347</b>
			3.1.1.72		
xylanase II		<i>Streptomyces thermoviolaceus</i>	3.2.1.8	D85897 BAA19778.1	<b>O08346</b>
chitin-binding protein celS2		<i>Streptomyces viridosporus</i>	none	AF126376 <b>AAD27623.1</b>	Q9X5K8
endo-1,4-glucanase S1		<i>Streptomyces viridosporus</i>	3.2.1.4	AF130408 <b>AAD25090.1</b>	
xylanase (SvxA)		<i>Streptomyces viridosporus</i>	3.2.1.8	AF198618 <b>AAF09501.1</b>	
ORF slr0897		<i>Synechocystis</i> sp. PCC 6803	n.d.	D64003 BAA10447.1	<b>Q55365</b>
				NC_000911.1 NP_442377.1	
cellobiohydrolase E3	<i>Cel6B</i>	<i>Thermobifida fusca</i>	3.2.1.91	U18978 AAA62211.1	<b>Q60029</b>
endo-1,4-glucanase E1	<i>Cel9B</i>	<i>Thermobifida fusca</i>	3.2.1.4	L20094 AAC06387.1	<b>Q08166</b>
endo-1,4-glucanase E2	<i>Cel6A</i>	<i>Thermobifida fusca</i>	3.2.1.4	M73321 AAC06388.1	<b>P26222</b> 3D
endo-1,4-glucanase E5	<i>Cel5A</i>	<i>Thermobifida fusca</i>	3.2.1.4	L01577 AAC09379.1	<b>Q01786</b>
endo/exo-1,4-glucanase E4	<i>Cel9A</i>	<i>Thermobifida fusca</i>	3.2.1.4	L20093 AAB42155.1	<b>P26221</b> 3D
			3.2.1.91		<b>Q08167</b>
exocellulase E6 (CelF)	<i>Cel48A</i>	<i>Thermobifida fusca</i>	3.2.1.91	AF144563 <b>AAD39947.1</b>	
xylanase		<i>Thermobifida fusca</i>	3.2.1.8	U01242 AAA21480.1	<b>Q56265</b>
chitinase A		<i>Thermococcus kodakaraensis</i>	3.2.1.14	<b>T43916</b>	
xylanase		<i>Thermomonospora alba</i>	3.2.1.8	Z81013 CAB02654.1	<b>P74912</b>
unnamed protein product		unidentified	n.d.	AX565635 <b>CAD58415.1</b>	
Sequence 2 from patent US 6207436		Unknown.	n.d.	<b>AAE63612.1</b>	
ORF EngXCA		<i>Xanthomonas axonopodis</i> pv. citri str. 306	n.d.	AE011689 <b>AAM35501.1</b>	
				NC_003919 NP_640965.1	
endo-1,4-glucanase		<i>Xanthomonas campestris</i>	3.2.1.4	M32700 AAA27612.1	P19487
				AJ304415 <b>CAC18529.1</b>	
EngXCA		<i>Xanthomonas campestris</i> pv. campestris str. ATCC 33913	n.d.	AE012472 <b>AAM42791.1</b>	
				NC_003902 NP_638867.1	
ORF XF0818		<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003921 <b>AAF83628.1</b>	Q9PF60
				NC_002488 NP_298108.1	
ORF XF1267		<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003960 <b>AAF84076.1</b>	Q9PDW2
				NC_002488 NP_298556.1	
EngXCA		<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012560 <b>AAO29683.1</b>	
				NC_004556 NP_780034.1	
GuxA		<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012555 <b>AAO28402.1</b>	
				NC_004556 NP_778753.1	

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# CAZy - Carbohydrate-Active enZYmes

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## Citing CAZy

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We are working hard at putting together and maintaining this server for the scientific community. If you found this server useful for your research we would appreciate if you cite CAZy(ModO). There are several ways to cite CAZy(ModO) (see below).

### 1. Mention this server name and URL:

Coutinho, P.M. & Henrissat, B. (1999) Carbohydrate-Active Enzymes server at  
URL: <http://afmb.cnrs-mrs.fr/~cazy/CAZY/index.html>

### 2. Quote papers where CAZy(ModO) is revealed:

Coutinho, P.M. & Henrissat, B. (1999) Carbohydrate-active enzymes: an integrated database approach. In *"Recent Advances in Carbohydrate Bioengineering"*, H.J. Gilbert, G. Davies, B. Henrissat and B. Svensson eds., The Royal Society of Chemistry, Cambridge, pp. 3-12.

Coutinho, P.M. & Henrissat, B. (1999) The modular structure of cellulases and other carbohydrate-active enzymes: an integrated database approach. In *"Genetics, Biochemistry and Ecology of Cellulose Degradation"*, K. Ohmiya, K. Hayashi, K. Sakka, Y. Kobayashi, S. Karita and T. Kimura eds., Uni Publishers Co., Tokyo, pp. 15-23.

### 3. Quote the references concerning the family classification(s) in question:

Glycosidases and Transglycosidases (or Glycoside Hydrolases)

Glycosyltransferases

Polysaccharide Lyases (*cite CAZyModO*)


Carbohydrate Esterases (*cite CAZyModO*)

Carbohydrate-Binding Modules

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## Swiss-Prot: P22533

*NiceProt - a user-friendly view of this Swiss-Prot entry*

ID MANB\_CALSA STANDARD; PRT; 1331 AA.  
 AC P22533;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-mannanase/endoglucanase A precursor [Includes: Mannan endo-1,4-  
 DE beta-mannosidase A (EC 3.2.1.78) (Beta-mannanase) (Endo-1,4-  
 DE mannanase); Endo-1,4-beta-glucanase (EC 3.2.1.4) (Cellulase)].  
 GN MANA.  
 OS *Caldocellum saccharolyticum* (*Caldicellulosiruptor saccharolyticus*).  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;  
 OC *Caldicellulosiruptor*.  
 OX NCBI\_TaxID=44001;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93119139; PubMed=1476429; [NCBI, ExPASy, EBI, Israel, Japan]  
 RA Gibbs M.D., Saul D.J., Luthi E., Bergquist P.L.;  
 RT "The beta-mannanase from '*Caldocellum saccharolyticum*' is part of a  
 RT multidomain enzyme.";  
 RL Appl. Environ. Microbiol. 58:3864-3867(1992).  
 RN [2]  
 RP SEQUENCE OF 1-346 FROM N.A.  
 RX MEDLINE=91247819; PubMed=2039230; [NCBI, ExPASy, EBI, Israel, Japan]  
 RA Luethi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;  
 RT "Cloning, sequence analysis, and expression in *Escherichia coli* of a  
 RT gene coding for a beta-mannanase from the extremely thermophilic  
 RT bacterium '*Caldocellum saccharolyticum*'.";  
 RL Appl. Environ. Microbiol. 57:694-700(1991).  
 CC -!- FUNCTION: DEGRADATION OF HEMICELLULOSES, THE SECOND MOST ABUNDANT  
 CC POLYSACCHARIDES IN NATURE. CONTAINS TWO CATALYTIC DOMAINS WITH  
 CC MANNANASE AND ENDOGLUCANASE ACTIVITIES.  
 CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic  
 CC linkages in mannans, galactomannans, glucomannans, and  
 CC galactoglucomannans.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.  
 CC -!- MISCELLANEOUS: THIS ENZYME IS MOST ACTIVE AT PH 6 AND 80 DEGREES  
 CC CELSIUS.  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY  
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).  
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY  
 CC J (FAMILY 44 OF GLYCOSYL HYDROLASES).  
 CC -----  
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 DR EMBL; L01257; AAA71887.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]  
 DR EMBL; M36063; AAA72861.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]  
 DR PIR; B43745; B43745.  
 DR PIR; A48954; A48954.  
 DR HSSP; Q06851; 1NBC. [HSSP ENTRY / SWISS-3DIMAGE / PDB]  
 DR InterPro; IPR001956; CBD 3.  
 DR InterPro; IPR001547; Glyco hydro 5.  
 DR InterPro; Graphical view of domain structure.  
 DR Pfam; PF00150; cellulase; 1.  
 DR Pfam; PF00942; CBM 3; 2.  
 DR ProDom; PD001947; CBD 3; 2.  
 DR ProDom [Domain structure / List of seq. sharing at least 1 domain]  
 DR PROSITE; PS00659; GLYCOSYL HYDROL F5; 1.  
 DR BLOCKS; P22533.  
 DR ProtoNet; P22533.  
 DR ProtoMap; P22533.  
 DR PRESAGE; P22533.  
 DR DIP; P22533.  
 DR ModBase; P22533.  
 DR SWISS-2DPAGE; GET REGION ON 2D PAGE.  
 KW Hydrolase; Glycosidase; Cellulose degradation; Signal;  
 KW Multifunctional enzyme.  
 FT SIGNAL 1 41 POTENTIAL.  
 FT CHAIN 42 1331 BETA-MANNANASE/ENDOGLUCANASE A.  
 FT DOMAIN 42 325 CATALYTIC (MANNANASE ACTIVITY). *GHS*  
 FT DOMAIN 326 361 PRO/SER/THR-RICH (PT BOX).  
 FT DOMAIN 362 518 *=156* SUBSTRATE-BINDING (POTENTIAL). *CBD II*  
 FT DOMAIN 519 564 PRO/SER/THR-RICH (PT BOX).  
 FT DOMAIN 565 720 *=155* SUBSTRATE-BINDING (POTENTIAL). *CBD II*  
 FT DOMAIN 721 780 PRO/SER/THR-RICH (PT BOX).  
 FT DOMAIN 781 1331 CATALYTIC (ENDOGLUCANASE ACTIVITY).  
 FT ACT\_SITE 162 162 PROTON DONOR (BY SIMILARITY).  
 FT ACT\_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).  
 FT CONFLICT 338 338 T -> P (IN REF. 2).  
 FT CONFLICT 340 346 TPTPTPT -> RQHQRQ (IN REF. 2).  
 SQ SEQUENCE 1331 AA; 146892 MW; FFBCA51BB8D8F0E0 CRC64;  
 MRLKTKIRKK WLSVLCTVVF LLNILFIANV TILPKVGAAT SNDGVVKIDT STLIGTNHAH  
 CWYRDRDLTA LRGISRSGMN SVRVVLSNGY RWTKIPASEV ANIISLSRSL GFKAIILEVH  
 DTTGYGEDGA ACSLAQAVEY WKEIKSVLDG NEDFVIINIG NEPYGNNNYQ NWVNDTKNAI  
 KALRDAGFKH TIMVDAPNWG QDWSNTMRDN AQSIMEADPL RNLVFSIHMY GVYNTASKVE  
 EYIKSFVDKG LPLVIGFEGH QHTDGDPEDE AIVRYAKQYK IGLFSWSWCG NSSYVGYLDM  
 VNNWDPNNPT PWGQWYKTNA IGTSSTPTPT STVTPTPTPT PTPTPTVTAT PTPTPTPVST  
 PATSGQIKVL YANKETNSTT NTIRPWLKVV NSGSSSIDLS RVTIRYWYTV DGERAQSAIS  
 DWAQIGASNV TFKFVKLSSS VSGADYYLEI GFKSGAGQLQ PGKDTGEIQM RFNKDDWSNY  
 NQGNDWSWIQ SMTSYGENEK VTAYIDGVLV WGQEPGATP APAPTATPTP TPTVTPTPTV  
 TPTPTVTATP TPTPTPTPTP VSTPATGGQI KVLANKETN STTNTIRPWL KVVNSGSSSI  
 DLSRVTIYRW YTV DGERAQS AISDWAQIGA SNVTFKFVKL SSSVSGADYY LEIGFKSGAG  
 QLQPGKDTGE IQIRFNKSDW SNYNQGNDSW WIQSMTSYGE NEKVYAYIDG VLVWGQEPG  
 TTPSPTSTPT VVTPTPTPTPT PTPTPTPTPT PTPTVTPTPT VTATPTPTPT PIPTVTPLPT  
 ISPPSPVVEI TINTNAGRTQ ISPYIYGANQ DIEGVVHSAR RLGGNRLTGY NWENNFSNAG  
 NDWYHSSDDY LCWSMGISSG DAKVPAAVVS KFHEYSLKNN AYSATVLTQMA GYVSKDNYGT  
 VSENETAPSN RWAIEVKFKKD APLSLNPDLN DNFVYMDEFI NYLINKYGMA SSPTGIKGYI  
 LDNEPDLWAS THPRIHPNKV TCKELIEKSV ELAKVIKTLT PSAEVFGYAS YGFMGYYSLO  
 DAPDWNQVKG EHRWFISWYL EQMKKASDSF GKRLLDVLDL HWYPEARGGN IRVCFDGEN  
 TSKEVVIARM QAPRTLWDPT YKTSVKGQIT AGENSWINQW FSDYLPPIPN VKADIEKYYP  
 GTKLAISEFD YGGRNHISGG IALADVLGIF GKYGVNFAAR WGDGSGSYAAA AYNIIYLNLYDG

KGSKYGNTNV SANTSDVENM PVYASINGQD DSELHIILIN RNYDQKLQVK INITSTPKYT  
KABIYGFDSN SPEYKMGNI DNIESNVFTL EVPKFNGVSH SITLDFNVI KIIQNEVIKF  
IRNLVFMRAL V

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